

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:23:41 ; Search time 30.25 Seconds

(without alignments)
1721.371 Million cell updates/sec

Title: US-09-522-278B-12

Perfect score: 1561

Sequence: 1 MTSRRSVKSGPPEVPRDEYE.....PTERRAPARCSAPRRPVE 301

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

```

1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-vertebrate:*
15: SP-virus:*
16: SP-bacteriophage:*
17: SP-archaeal:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014.5	65.0	300	12	P89468 herpes simp
2	270.5	17.3	304	12	O39253 equine herp
3	228	14.6	301	12	O9E206 cercopithec
4	210	13.5	249	12	O69318 marek's dis
5	210	13.5	249	12	O9E206 cercopithec
6	207	13.3	241	12	O89247 turkey herp
7	198	12.7	283	12	O9DHC2 gallid herp
8	168.5	10.8	388	4	O9NY42 meleagrid h
9	168.5	10.8	441	4	O75685 homo sapien
10	153	9.8	252	12	O9DMG9
11	149.5	9.6	956	4	O9UQ39
12	149.5	9.6	2752	4	O9UQ35
13	149.5	9.6	3122	12	P89459
14	148	9.5	266	12	O56868 gallid herp
15	146.5	9.4	395	16	O9RV74
16	146.5	9.4	1343	4	O9H7N4

17	146	9.4	839	16	O9RX57	O9rx57 delinococcus
18	146	9.4	1262	4	O9UQ40	O9uq40 homo sapien
19	144	9.2	1037	16	O9AC25	O9ac25 caulobacter
20	144	9.2	1201	10	O9C651	O9c651 arabidopsis
21	143.5	9.2	889	4	O9UL51	O9ul51 homo sapien
22	143.5	9.2	1154	4	O9P2P0	O9p2p0 homo sapien
23	142	9.1	1249	5	O9N8G4	O9n8g4 trypanosoma
24	140.5	9.0	1265	3	O5N920	O5n920 pneumocysti
25	140.5	9.0	1992	3	O9P6T1	O9p6t1 neurospora
26	140	9.0	1132	16	O9PRC7	O9prc7 delinococcus
27	139.5	8.9	932	5	O93562	O93562 caenorhabdit
28	139	8.9	438	16	O9A2W5	O9a2w5 caulobacter
29	138.5	8.9	1312	4	O9NR59	O9nr59 homo sapien
30	137	8.8	590	2	O9S205	O9s205 streptomyces
31	137	8.8	797	2	O9RKS9	O9rks9 streptomyces
32	137	8.8	835	2	O9K3E2	O9k3e2 streptomyces
33	137	8.8	1069	12	O6Y140	O6y140 human herpe
34	136.5	8.7	694	6	O9GKY7	O9gky7 oryctolagus
35	136.5	8.7	889	4	O9UBS2	O9ubs2 homo sapien
36	136.5	8.7	1320	11	O08784	O08784 mus musculus
37	136	8.7	212	11	O70446	O70446 mus musculus
38	136	8.7	436	4	O9ES01	O9es01 homo sapien
39	136	8.7	2936	5	O9NKP7	O9nkp7 leishmania
40	135.5	8.7	612	2	O9Z614	O9z614 streptomyces
41	135.5	8.7	1175	6	O9TV66	O9tv66 oryctolagus
42	134	8.6	667	11	O9R1D9	O9r1d9 mus musculus
43	134	8.6	721	4	O9E648	O9e648 homo sapien
44	134	8.6	737	11	O9WVF3	O9wvf3 mus musculus
45	134	8.6	806	11	O9WVF4	O9wvf4 mus musculus

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	300 AA.
1	P89468			
AC	P89468:			
DT	01-MAY-1997 (TREMBLrel. 03, Created)			
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	TEGUMENT PROTEIN.			
GN	UL49.			
OS	Herpes simplex virus (type 2).			
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
OX	Alphaherpesvirinae; Simplexvirus.			
NCBI_TaxID=10310;				
[1]	SEQUENCE FROM N.A.			
RP	STRAIN-HG52:			
RC	MEDLINE-87111457; PubMed-3027242;			
RA	McGeoch D.J., Moss H.W., McNab D., Frame M.C.;			
RT	"DNA sequence and genetic content of the HindIII 1 region in the short			
RT	unique component of the herpes simplex virus type 2 genome:			
RT	identification of the gene encoding glycoprotein G, and evolutionary			
RT	comparisons."			
U. Gen. Virol. 68:19-38(1987).				
[2]	SEQUENCE FROM N.A.			
RP	STRAIN-HG52:			
RC	MEDLINE-90278430; PubMed-2161906;			
RX	Everett R., Fenwick M.;			
RA	"Comparative DNA sequence analysis of the host shut-off genes of			
RT	different strains of herpes-simplex virus: type 2 strain HG52 encodes			
RT	a truncated UL41 product."			
U. Gen. Virol. 71:1387-1390(1998).				
[3]	SEQUENCE FROM N.A.			
RP	STRAIN-HG52:			
RC	MEDLINE-92113549; PubMed-1662697;			
RA	McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;			
RT	"Comparative sequence analysis of the long repeat regions and			
RT	adjointing parts of the long unique regions in the genomes of herpes			

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RT simplex viruses types 1 and 2."
RL J. Gen. Virol. 72:3057-3075(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-HG52:
RX MEDLINE-92356101; PubMed-1322965;
RA Bernick B.C., Dolan A., Telford E.A.R., Davison A.J., McGeoch D.J.;
RT "A novel herpes simplex virus gene (UL49A) encodes a putative membrane
protein with counterparts in other herpesviruses.";
RL J. Gen. Virol. 73:2167-2171(1992).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-HG52:
RA Dolan A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z86099; CAB06735.1; -.
SO SEQUENCE 300 AA; 31790 MW; FC72D09F7FB7B096 CRC64;

Query Match 65.0%; Score 1014.5; DB 12; Length 300;
Best Local Similarity 69.2%; Pred. No. 1.3e-62;
Matches 209; Conservative 19; Mismatches 71; Indels 3; Gaps 3;

QY 1 MTSRSVSKSGPREVPREDYEDLYTTPSSGMASSPSPDTSRGA LQTRSRQGEVRFVQ 60
DB 1 MTSRSVSKSGPREVPREDYEDLYTTPSSGMASSPSPDTSRGA LQTRSRQGEVRFVQ 59
QY 61 DESDYALYGGSSSEDDHEHVEVPTRRPVSGAVLSGPGPARAPPPAGSGGA-GRTPTTAP 119
DB 60 DESDYALYGGSSSEDDHEHVEVPTRRPVSGAVLSGPGPARAPPPAGSGGA-GRTPTTAP 119
QY 120 RAPRTORVATKAPAPAEETTRGRKSAOPESALPDAPASTAPTRSKTPAOG LKHLFS 179
DB 120 RAPRTORVATKAPAPAEETTRGRKSAOPESALPDAPASTAPTRSKTPAOG LKHLFS 179
QY 180 TAPNPAPAPPTPRVAGFNKRVFCAGVRLAAMHARMAAVQ LMDMSRRTDDELLELGIT 239
DB 180 TAPNPAPAPPTPRVAGFNKRVFCAGVRLAAMHARMAAVQ LMDMSRRTDDELLELGIT 239
QY 240 TIRTVCEGNLLO RANELVNDVVDVDAATATRGSAASRPERRPARASASRRRP 299
DB 240 TIRTVCEGNLLO RANELVNDVVDVDAATATRGSAASRPERRPARASASRRRP 299
QY 300 VE 301
DB 299 LE 300

RESULT 2
039253 PRELIMINARY; PRT; 304 AA.
AC 039253:
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE COUNTERPART OF HSV-1 GENE UL49 AND VZV GENE 9.
GN 11.
OS Equine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10331;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NS80567;
RX MEDLINE-94058670; PubMed-8240007;
RA Riggall M., Onions D.E.;
RT "DNA sequence of a gene cluster in the equine herpesvirus-4 genome
which contains a newly identified herpesvirus gene encoding a membrane
protein.";
RL Arch. Virol. 133:171-178(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-NS80567;

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RX MEDLINE-98264497; PubMed-9603335;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-4.";
RL J. Gen. Virol. 79:1197-1203(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-NS80567;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030027; AAC59525.1; -.
SO SEQUENCE 304 AA; 33483 MW; 07A8725F7774FC43 CRC64;

Query Match 17.3%; Score 270.5; DB 12; Length 304;
Best Local Similarity 34.4%; Pred. No. 2.4e-11;
Matches 85; Conservative 18; Mismatches 77; Indels 67; Gaps 11;

QY 60 YDESDYALYGGSSSEDDHEHVEVPTRRPVSGAVLSGCG---PARAPPPAGSGAGRTPT 116
DB 98 YDACEYSLVGG-----GKLTSHGRUSPTKTHPK---SAGVTP- 134
QY 117 TAPAPRTORVATKAPAPAEETTRGRKSAOPESALPDAPASTAPTRSKTPAOG L--AR 174
DB 135 -----PQRY-----PARPAT-----RAAP--SATPTQPCYAKQRTSPGVNSTRSGK 175
QY 175 KLHSTAPNPNDAPWTBPRVAGFNKRVFCAGVRLAAMHARMAAVQ LMDMSRPTDDELNE 234
DB 176 SLAFSCPTKPKPTKPTWYGATLFFKNVFCAAVSRVAALHAASDAALMDLPKPTNEGLDR 235
QY 235 LLGTTIRVYCEGNLLO RANELVNDVVDVDAATATRRS---AASPTRRPAPA 290
DB 236 FLKAAARILVCEGSKLLEMAN-----ATMERSPDGAAAVAPIGYDRRP- 279
QY 291 RSASRR 297
DB 280 RLASRRR 286

RESULT 3
09E206 PRELIMINARY; PRT; 301 AA.
AC 09E206:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOHETICAL 33.2 KDA PROTEIN.
OS Cercarial dermatitis virus 7.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=35245;
RN [1]
RP SEQUENCE FROM N.A.
RA Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
RT "Complete sequence of the Simian Varicella Virus Genome.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF275348; AAC27246.1; -.
KW Hypothetical protein.
SO SEQUENCE 301 AA; 33161 MW; A451C74ADC844A02 CRC64;

Query Match 14.6%; Score 228; DB 12; Length 301;
Best Local Similarity 26.1%; Pred. No. 2e-08;
Matches 91; Conservative 26; Mismatches 86; Indels 146; Gaps 14;

QY 4 RRSVSKSGPREVPREDYEDLYTTPSSGMASSPSPDTSRGA LQTRSRQGEVRFVQ 59
DB 39 RRSVVG---FPDSDSLGLYAT---VETESPLFYGDVS--GTVDKR-----HTMIS 85
QY 60 YDESDYALYGGSSSEDDHEHVEVPTRRPVSGAVLSGCG---PARAPPPAGSGAGRTPT 116
DB 86 NNSSD-----SDDFEDIDEVIAAFKARLKHENHEDAVYENVOGNAQPMIOKHN 137
QY 86 RPSGAVLSGPGPARAPPPAGSGAGRTPTTAPRAPRTORVATKAPAPAEETTRGRKS 145

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Db 138 RDVD-----SEKRAP-----GAG-----151
Oy 146 ACPESALADPASTAPTSTKTPAOGCLAKHSTAPRNPDAWTPRVAGFNKRVCAAV 205
Db 152 -----ALASGRPLSESTAPKNTTSACGPTPAYNRYCEAI 188
Oy 206 GRLLAAHMAAVALMDMSRPTDEDNLGTTTIRVYCEGKNLLOANELV---NDP 262
Db 189 RRIIAAQOARAAEAAMSSNPPRNNAELDLRLAGTVYRITVHEGSLNIQVANDLELGGKPD 248
Oy 263 -----VVQDYDAATATATGRSASRPT-----RRAPASASRP 296
Db 249 RKOSTARRKKEIYKOTDDEPYVAQVAKINSRGTPVSGTSRARTSRVSKP 297

RESULT 4
Oy 069318 PRELIMINARY: PRT: 249 AA.
AC 069318:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE UL49H.
GN UL49H.
OS Marek's disease herpesvirus (strain GA) (MDHV), and
OS Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10388, 10390;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=chicken herpesvirus 1, and Turkey herpesvirus; STRAIN=GA;
RA MEDLINE=93389438; PubMed=8397281;
RA Yanagida N., Yoshida S., Nazerian K., Lee L.F.;
RT "Nucleotide and predicted amino acid sequences of Marek's disease
RT virus homologues of herpes simplex virus major tegument proteins.";
RL J. Gen. Virol. 74:1837-1845(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Turkey herpesvirus; STRAIN=GA;
RA MEDLINE=92237304; PubMed=1315048;
RA Jones D., Lee L., Liu J.L., Kung H.J., Tillotson J.K.;
RT "Marek disease virus encodes a basic-leucine zipper gene resembling
RT the fos/jun oncogenes that is highly expressed in lymphoblastoid
RT tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Turkey herpesvirus; STRAIN=GA;
RA Lee L.F., Wu P., Sul D., Ren D., Kung H.J.;
RT "The complete UL sequence of Serotype I Marek's disease virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
DR EMBL: L10283; AAA03148.1;
DR EMBL: AF147806; AAF66784.1;
SQ SEQUENCE 249 AA; 27656 MW; B251007B6720F651 CRC64;

Query Match 13.5%; Score 210; DB 12; Length 249;
Best Local Similarity 25.9%; Pred. No. 2.9e-07;
Matches 74; Conservative 33; Mismatches 93; Indels 86; Gaps 9;

Oy 38 DTSRRGALOTRSRQREVFYQYDESDVALYGSSEDEDEHEVP-----RTRRPVSA 91
Db 3 DSERRKSEERRS-----LGPSAYDD--VSIARRSTRTQRNLND 42
Oy 92 VLSGPGAPARAPPAGSGAGRTPTTAPRAPRTOR-VATKAPAAPAAETTRGRKSAOPES 150
Db 43 DLSKHGPFTHDP-----TQKHSAKAVSEDVSTTRGGFTKRP-- 80
Oy 151 AALPDAPASTAPTSTKTPAOGCL-ARKLHSTAPRNPDAWTPRVAGFNKRVCAAVGRLA 209
Db 81 -----RTKPGVRAVQSNKFASFSTAPSSASTWRSNTVAFNORMCGAVATVA 127

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Oy 210 AMHARAAVALMDMSRPTDEDNLGTTTIRVYCEGKNL-----LQ 253
Db 128 QTHAYGALALMRQDPPRTNEELDAFLSRAVYKTIITQEGPNLMGEAETCARLLSESGLS 187
Oy 254 RANELVNPVVDVDAATATRG-----RSASRPTERRAPARS 292
Db 188 QGSENVKSKSERTTKSERTTRGGEIEIKSPDPSHHTHNPRTPAT 233

RESULT 5
Oy 09E6M7 PRELIMINARY: PRT: 249 AA.
AC 09E6M7:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE UL49 TEGUMENT PHOSPHOPROTEIN-LIKE PROTEIN.
GN MDV062.
OS Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
OX NCBI_TaxID=10390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MD5;
RA MEDLINE=20392152; PubMed=10933706;
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RT "The genome of a very virulent Marek's disease virus.";
RL J. Virol. 74:7980-7988(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MD5;
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RT Submitted (MAR-2000) to the EMBL/Genbank/DDOJ databases.
RL EMBL: AF243438; AAG14242.1;
SQ SEQUENCE 249 AA; 27626 MW; 58F00BCB7631F65D CRC64;

Query Match 13.5%; Score 210; DB 12; Length 249;
Best Local Similarity 25.9%; Pred. No. 2.9e-07;
Matches 74; Conservative 33; Mismatches 93; Indels 86; Gaps 9;

Oy 38 DTSRRGALOTRSRQREVFYQYDESDVALYGSSEDEDEHEVP-----RTRRPVSA 91
Db 3 DSERRKSEERRS-----LGPSAYDD--VSIARRSTRTQRNLND 42
Oy 92 VLSGPGAPARAPPAGSGAGRTPTTAPRAPRTOR-VATKAPAAPAAETTRGRKSAOPES 150
Db 43 DLSKHGPFTHDP-----TQKHSAKAVSEDVSTTRGGFTKRP-- 80
Oy 151 AALPDAPASTAPTSTKTPAOGCL-ARKLHSTAPRNPDAWTPRVAGFNKRVCAAVGRLA 209
Db 81 -----RAKPGVRAVQSNKFASFSTAPSSASTWRSNTVAFNORMCGAVATVA 127
Oy 210 AMHARAAVALMDMSRPTDEDNLGTTTIRVYCEGKNL-----LQ 253
Db 128 QTHAYGALALMRQDPPRTNEELDAFLSRAVYKTIITQEGPNLMGEAETCARLLSESGLS 187
Oy 254 RANELVNPVVDVDAATATRG-----RSASRPTERRAPARS 292
Db 188 QGSENVKSKSERTTKSERTTRGGEIEIKSPDPSHHTHNPRTPAT 233

RESULT 6
Oy 089247 PRELIMINARY: PRT: 241 AA.
AC 089247:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE TEGUMENT PROTEIN (UL49 PROTEIN).
GN UL49 OR ORF 57.
OS Gallid herpesvirus 1 (serotype 2), and

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OY		23	YTPPSSGMAEPDSEPPMISRKCALOTRSRQGEAFVFIYDESDALYGGSSSEDDEHNEVP	82
	I I I I I		I I I I I	
Db		77	YGSAFAAGAA---ADTAAARAAPA-----DPD---SGATPEPDSTGAP	116
	I I I I I		I I I I I	
OY		83	RTRRPVSGLVIGCFPARAPPAA--GSGGAGRTPT----TAPRAER--TORVATATA	133
	I I I I I		I I I I I	
Db		117	AD--PDGGAAGAADDSCGAAPAAPADPDPSGAAPDAADPDGGAAPDAADPDGACGAAPAPA	174
	I I I I I		I I I I I	

Db 194 -----DPD-----GRTSGSRSGT PRCPSRAASRPPGGRSRRTRP

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RESULT 11
ID 090039 PRELIMINARY: PRT: 956 AA.
AC 090039:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RNA BINDING PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Ohtaki S., Umeki K., Sawada Y.;
RT "Homo sapiens mRNA for RNA binding protein, partial cds.:"
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016088; BAA83714.1;
DR InterPro: IPR002965; P_rich_extensn.
DR PRINTS: PRO1217; PRICEXTENS.
FT NON_TER 1 1
FT 956 956
SQ SEQUENCE 956 AA: 106462 MW: C9FEAD07B49F5011 CRC64;

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Query Match          9.6%; Score 149.5; DB 4; Length 956;
Best Local Similarity 21.7%; Pred. No. 0.019;
Matches 86; Conservative 47; Mismatches 109; Indels 155; Gaps 19;

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QY 4 RRSVKSQPR-----EYPRDEYEDLY-----TPSSGMASSPDSPPTSRGALQTRS 49
   ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 163 RRESSSPRRERKSSKKKKHRESESKKKHRSPTPKSKKDKKKRSTTPAPKS 222
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 50 RQGEVRFVQYDSDVLYGSSSEDDENHEVPRTRPVSGA-----VLSGPPAPAPPP 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 223 RR-----AHNSTADSNSSDTSRSRSRAAATHTTALAG-----NSPSP 263
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 105 PAGSGAGRT-----TTAPRAPRTQVATKAPAPAEETTRGRK-----SAQPE-SA 151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 264 ASGRRGEGDAPFSEPGTTSTQRPSSPETATKQPSPEEDKDKKKSATRPSPERRSS 323
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 152 ALPDAPAST-----APTRSKTPAAG--LARKLHF 178
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 324 TGEPPAPPTPLLAERHGGSPQPLATTPLSQEPVNPPEASPTDRSPKSPKLPQSSSS 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 179 STAPPNP-----DAPWTPRVA---GFNKRVCFAVGRLAAMHARAAVQLMDMSR 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 384 ESSPSPQPTKVRHASSSPESPAPAPAPGSHREISSPTSKNRS-HGRAKR---DKSH 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 226 PRTEDELNELLGITTRVTCGEGKNLLQRLANELVNPVDVDAATATGRSAASRPT- 284
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 439 SHTPS-----RMRGRSRP-----ATKKRGRSRSRPTTKR 468
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 285 ---RPRAP---ARSASR-----PRRP 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 469 GHSRSPSPQWRRSRSPQWRGSRSPQWRGRSRSPOR 505
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 12
ID 090035 PRELIMINARY: PRT: 2752 AA.
AC 090035:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RNA BINDING PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Ohtaki S., Umeki K., Sawada Y.;

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RT "Homo sapiens mRNA for RNA binding protein, complete cds.:"
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016092; BAA83718.1;
DR InterPro: IPR002965; P_rich_extensn.
DR PRINTS: PRO1217; PRICEXTENS.
SQ SEQUENCE 2752 AA: 299672 MW: 109C64F181097123 CRC64;

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Query Match          9.6%; Score 149.5; DB 4; Length 2752;
Best Local Similarity 21.7%; Pred. No. 0.06;
Matches 86; Conservative 47; Mismatches 109; Indels 155; Gaps 19;

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QY 4 RRSVKSQPR-----EYPRDEYEDLY-----TPSSGMASSPDSPPTSRGALQTRS 49
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DB 198 RRESSSPRRERKSSKKKKHRESESKKKHRSPTPKSKKDKKKRSTTPAPKS 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 50 RQGEVRFVQYDSDVLYGSSSEDDENHEVPRTRPVSGA-----VLSGPPAPAPPP 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 258 RR-----AHNSTADSNSSDTSRSRSRAAATHTTALAG-----RSPSP 298
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QY 105 PAGSGAGRT-----TTAPRAPRTQVATKAPAPAEETTRGRK-----SAQPE-SA 151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 299 ASGRRGEGDAPFSEPGTTSTQRPSSPETATKQPSPEEDKDKKKSATRPSPERRSS 358
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 152 ALPDAPAST-----APTRSKTPAAG--LARKLHF 178
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DB 359 TGEPPAPPTPLLAERHGGSPQPLATTPLSQEPVNPPEASPTDRSPKSPKLPQSSSS 418
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 179 STAPPNP-----DAPWTPRVA---GFNKRVCFAVGRLAAMHARAAVQLMDMSR 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 419 ESSPSPQPTKVRHASSSPESPAPAPAPGSHREISSPTSKNRS-HGRAKR---DKSH 473
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QY 226 PRTEDELNELLGITTRVTCGEGKNLLQRLANELVNPVDVDAATATGRSAASRPT- 284
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DB 474 SHTPS-----RMRGRSRP-----ATKKRGRSRSRPTTKR 503
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QY 285 ---RPRAP---ARSASR-----PRRP 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 504 GHSRSPSPQWRRSRSPQWRGSRSPQWRGRSRSPOR 540
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RESULT 13
ID P89459 PRELIMINARY: PRT: 3122 AA.
AC P89459:
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VERY LARGE TEGUMENT PROTEIN.
GN UL36.
OS Herpes simplex virus (type 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10310;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=HG52;
RX MEDLINE=87111457; PubMed=3027242;
RA McGeoch D.J., Moss H.W., McNab D., Frame M.C.;
RT "DNA sequence and genetic content of the HindIII 1 region in the short
RT unique component of the herpes simplex virus type 2 genome:
RT identification of the gene encoding glycoprotein G, and evolutionary
RT comparisons.:"
RL J. Gen. Virol. 68:19-38(1987).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=HG52;
RX MEDLINE=90278430; PubMed=2161906;
RA Everett R., Fenwick M.;
RT "Comparative DNA sequence analysis of the host shutoff genes of
RT different strains of herpes simplex virus: type 2 strain HG52 encodes
RT a truncated UL41 product.:"
RL J. Gen. Virol. 71:1387-1390(1990).

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RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HG52;
 RX MEDLINE-92113549; PubMed-1662697;
 RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
 RT "Comparative sequence analysis of the long repeat regions and
 RT adjoining parts of the long unique regions in the genomes of herpes
 RT simplex viruses types 1 and 2."
 RL J. Gen. Virol. 72:3057-3075(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HG52;
 RX MEDLINE-92356101; PubMed-1322965;
 RA Barrett B.C., Dolan A., Telford E.A.R., Davidson A.J., McGeoch D.J.;
 RT "A novel herpes simplex virus gene (UL49) encodes a putative membrane
 RT protein with counterparts in other herpesviruses."
 RL J. Gen. Virol. 73:2167-2171(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HG52;
 RA Dolan A.;
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: Z86099; CAB06722.1; -
 DR InterPro: IPR001109; HupF_HypC.
 SQ SEQUENCE 3122 AA; 330045 MW; 6EBF94B51BE8C0B CRC64;

Query Match 9.6%; Score 149.5; DB 12; Length 3122;
 Best Local Similarity 26.1%; Pred. No. 0.069;
 Matches 74; Conservative 22; Mismatches 110; Indels 77; Gaps 11;

QY 75 DDEHEVPTRRRPVSGAVLSGPGAPARPPPGSGAGRPPTTAPRPTORVATK----- 130
 DB 2633 DDPREPPTRPPSPADAL-----PPPAFSGSAAFSAVPRVRSKRTRAKSRAP 2682
 QY 131 -----APAAPAETTR-GKRSAPESA-----ALPDPAST-----A 161
 DB 2683 RASAPPEGRRPALPAPVAPVAAASARPPDPTPESAPAMVASLPLPSPASARGAFPA 2742
 QY 162 PTRS---KTPAGCLA-----RKLHFTAPRPDAPWTPRVAGFKRVCAGLAAM 211
 DB 2743 PTLAPPPAPGCAVVGSGDRRRGRQTGSPPPRGP-AAAGPRRLTRPAVASLSA- 2800
 QY 212 HARMAVOLMDMSRPTDEDLNLGTTIRTVCEG-----KNLQRLANELVNP----- 262
 DB 2801 -----SINSLPSPRPDPADHAANAASAAAAPPSGLAPPTSAVOTSPPLAPGCVAPS 2853
 QY 263 -----VQDVDAATATGRSAASRPTERRAPARSASRRPR 299
 DB 2854 EPLCGWVPGPVARARPPQSPATKPAARTRIARNSVPPPLP 2896

RESULT 14
 O56868 PRELIMINARY; PRT; 266 AA.
 AC O56868;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE VIRAL TEGUMENT PROTEIN.
 GN UL49.
 OS gallid herpesvirus 1.
 OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 OX NCBI_TaxId=10386;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98080487; PubMed-9420298;
 RA Ziemann K., Mettenleiter T.C., Fuchs W.;
 RT "Gene arrangement within the unique long genome region of infectious
 RT latyngotracheitis virus is distinct from that of other
 RT alphaherpesviruses."
 RL J. Virol. 72:847-852(1998).

DR EMBL: Y14300; CAA74678.1; -
 DR InterPro: IPR001917; AminoTransf_2.
 DR PROSITE: PS00599; AA_TRANSFER_CLASS_2; UNKNOWN.1.
 SQ SEQUENCE 266 AA; 30358 MW; FF0459DAE1C6F4A9 CRC64;

Query Match 9.5%; Score 148; DB 12; Length 266;
 Best Local Similarity 21.6%; Pred. No. 0.0058;
 Matches 59; Conservative 33; Mismatches 113; Indels 68; Gaps 8;

QY 68 YGGSSEDEHPEVPRTRPPVSGAVLSGPGAPARPP----- 105
 DB 4 YDLSEAAKKYHDDTERRDDT-----TRRPQPQFHEPWSGSRRTSPYLDLRGSD 54
 QY 106 --AGSGAARTTTTARARTQVATKAPAAETTRKRSKQSPSALPDPASTAPT 163
 DB 55 SDSSEGDYH-----PSRAHYSRDHTAPP-----QGRSRPMSFKETTPKEEPPQ 101
 QY 164 RSK-----TPAQLARKLHF-----STAPPNDAPWTPRVAGFNKRVCAVGLAAMH 212
 DB 102 SKRGWNPDMHCAGIMRRLISKGFSGATPSGDEDPWHTSTIPANRSATVQAVSTAMQ 161
 QY 213 ARMAVOLMDMSRPTDEDLNLGTTIRTVCEGKNLQRLANELVNPVQVDDAATA 272
 DB 162 AELIAREVMDVTKPTNRELMDVRELFTIILNPGESLMS-----VATSVARAIEGTP 216
 QY 273 TGRSAASRPTERR-----APARSASRRPR 299
 DB 217 ITHELLOKRRSKPPTRKTEGARGSSSRSPQ 249

RESULT 15
 Q9RVT4 PRELIMINARY; PRT; 395 AA.
 AC Q9RVT4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HYPOHETICAL 40.0 KDA PROTEIN.
 GN DR0938.
 OC Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxId=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R1;
 RX MEDLINE-20036896; PubMed-10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Uitterback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1."
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001946; AAF10516.1; -
 DR TIGR: DR0938; -
 DR InterPro: IPR002965; P-rich_extensn.
 DR PRINTS: PR01217; PRICHEXTENS.
 KM Hypothetical protein: Complete proteome.
 SQ SEQUENCE 395 AA; 40003 MW; 75FD9637171DAAF0 CRC64;

Query Match 9.4%; Score 146.5; DB 16; Length 395;
 Best Local Similarity 25.1%; Pred. No. 0.011;
 Matches 80; Conservative 23; Mismatches 133; Indels 83; Gaps 13;
 QY 6 SVKSGPREVPDEYEDLYTPSSGMASSPDPSTSRGALQTRSGRGVRFVQYDESDY 65
 DB 44 SLLGERRAPAPVPG-----APQPTTSIPVSPGAVVADGSPQTAAPAOAQT----- 90

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OY 66 ALYGSSSEDEHPEVPRTRRPVSGAVLSGPGAPAPPPPPAGSGAGRTP-----TTAP 119
Db 91 ---AGKIPPAAPAPAPKIPPVLP-----PEPRRMPAPP-----TPPRPVEETTTA 133
OY 120 RAPRTORVATKAPA-----APAAETTRGRKSAOPESALPDAPASTARTRSKTPAQGL 172
Db 134 ASPTTQPPVTQAPATQTPTPTQTPAQAQAPATQPPATP--APEPAAPAEPAATTPPEPAT-- 189
OY 173 ARKLHSTAPPNPDAPWTPRVA-----GFNKRVECAVGRILAAHARMAAVQIWDMS 224
Db 190 -----PTEPAAP-APGTPAVAPSAQRTPLRSDYRVMLGTFGSEALRSATAGV----- 236
OY 225 RPRDDELNELGITTIRVTVCCKNLQR----ANELVNPVYQDYDAATATGRSAS 280
Db 237 -----SALGYTVYAI DL--GNOFVAQVGPFADEASGQAADIRRAYARARELYPPR 285
OY 281 RPTERRAPAPARSASRP RP 299
Db 286 GQTLRNPAPAAAABEAPATP 304
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Search completed: August 28, 2002, 12:27:39
Job time: 238 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:27:42 ; Search time 108.25 Seconds
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Title: US-09-522-278b-12

Perfect score: 1561

Sequence: 1 MTSRRSYKSGPREVDEYE.....PTERRPARASAPRRPE 301

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 2352106

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/paa/US06_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	11.5	37	13	US-08-902-572-16
2	179	11.5	37	14	US-09-063-657-18
3	179	11.5	37	17	US-09-320-912b-49
4	179	11.5	37	17	US-09-347-504-14
5	179	11.5	37	18	US-09-415-795-27
6	179	11.5	37	21	US-09-718-233-16
7	169	10.8	34	14	US-09-011-073-2

8	169	10.8	34	16	US-09-229-486-2	Sequence 2, Appl
9	169	10.8	34	21	US-09-773-430-2	Sequence 2, Appl
10	169	10.8	34	24	US-10-083-889-19	Sequence 19, Appl
11	166	10.6	34	21	US-09-780-070-39	Sequence 39, Appl
12	73	4.7	48	20	US-09-617-682A-15494	Sequence 13494, A
13	69.5	4.5	43	24	US-10-029-386-31973	Sequence 31973, A
14	68.5	4.4	48	22	US-09-880-578-32	Sequence 32, Appl
15	67.5	4.3	47	21	US-09-708-477-6419	Sequence 46419, A
16	65	4.2	49	22	US-09-855-754-14	Sequence 14, Appl
17	64.5	4.1	42	7	US-08-322-768A-23	Sequence 23, Appl
18	64.5	4.1	48	22	US-09-855-754-20	Sequence 20, Appl
19	64	4.1	48	1	PCR-US01-08631-35222	Sequence 35222, A
20	64	4.1	48	20	US-09-688-051-1876	Sequence 1876, Ap
21	64	4.1	50	1	PCR-US99-17738-21	Sequence 21, Appl
22	63	4.0	49	1	PCR-US97-14834-11	Sequence 11, Appl
23	63	4.0	49	13	US-08-916-246-11	Sequence 11, Appl
24	63	4.0	49	23	US-09-949-186-11	Sequence 11, Appl
25	62.5	4.0	43	20	US-09-617-681A-1322	Sequence 1322, Ap
26	62	4.0	35	14	US-09-050-861A-13	Sequence 13, Appl
27	62	4.0	45	15	US-09-192-433-56	Sequence 56, Appl
28	62	4.0	50	21	US-09-766-692-2303	Sequence 2303, Ap
29	61	3.9	50	26	US-60-213-162-126	Sequence 126, App
30	60.5	3.9	46	19	US-09-583-110-1648	Sequence 4648, Ap
31	60.5	3.9	48	1	PCR-US00-06830-133	Sequence 133, App
32	60.5	3.9	49	16	US-09-270-767-16437	Sequence 36437, A
33	60.5	3.9	49	16	US-09-270-767-51654	Sequence 51654, A
34	60.5	3.9	49	16	US-09-270-8498-185006	Sequence 185006, A
35	60	3.8	45	13	US-08-961-520-53	Sequence 53, Appl
36	60	3.8	45	21	US-09-708-427-45178	Sequence 45178, A
37	59	3.8	35	17	US-09-396-347B-11	Sequence 11, Appl
38	59	3.8	35	17	US-09-396-347B-42	Sequence 42, Appl
39	59	3.8	35	17	US-09-396-347D-11	Sequence 11, Appl
40	59	3.8	35	17	US-09-396-347D-42	Sequence 42, Appl
41	59	3.8	39	6	US-08-247-544-2	Sequence 2, Appl
42	59	3.8	50	21	US-09-708-427-57629	Sequence 57629, A
43	58.5	3.7	40	24	US-10-029-386-33404	Sequence 33404, A
44	58.5	3.7	42	22	US-09-855-754-23	Sequence 23, Appl
45	58.5	3.7	48	20	US-09-688-051-2166	Sequence 2166, Ap

ALIGNMENTS

RESULT 1
US-08-902-572-16
; Sequence 16, Application US/08902572
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jeno
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,572
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-069, 03

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-902-572-16

Query Match
Best Local Similarity 100.0%; Score 179; DB 13; Length 37;
Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DVDATATRGSAASRPTERRAPARSASRRPRVE 301
DB 2 DVDATATRGSAASRPTERRAPARSASRRPRVE 37

RESULT 2
US-09-063-657-18
; Sequence 18, Application US/09063657
; GENERAL INFORMATION:
; APPLICANT: Hannon, Gregory J.
; APPLICANT: Wang, Jing
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: EXTENSION OF CELLULAR LIFESPAN, METHODS AND REAGENTS
; FILE REFERENCE: CSV-008.01
; CURRENT APPLICATION NUMBER: US/09/063,657
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 37
; TYPE: PRT
; ORGANISM: HSV-1
; FEATURE:
; OTHER INFORMATION: VP22
; US-09-063-657-18

Query Match
Best Local Similarity 100.0%; Score 179; DB 14; Length 37;
Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DVDATATRGSAASRPTERRAPARSASRRPRVE 301
DB 2 DVDATATRGSAASRPTERRAPARSASRRPRVE 37

RESULT 3
US-09-320-912B-49
; Sequence 49, Application US/09320912B
; GENERAL INFORMATION:
; APPLICANT: Hannon, G.
; APPLICANT: Wang, J.
; APPLICANT: Beach, D.
; TITLE OF INVENTION: EXTENSION OF CELLULAR LIFESPAN, METHODS AND REAGENTS
; FILE REFERENCE: CSHL-P02-008
; CURRENT APPLICATION NUMBER: US/09/320,912B
; CURRENT FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/063,657
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; US-09-320-912B-49

Query Match
Best Local Similarity 100.0%; Score 179; DB 17; Length 37;
Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DVDATATRGSAASRPTERRAPARSASRRPRVE 301
DB 2 DVDATATRGSAASRPTERRAPARSASRRPRVE 37

RESULT 4
US-09-347-504-14
; Sequence 14, Application US/09347504
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/09/347,504
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VP22
; US-09-347-504-14

Query Match
Best Local Similarity 100.0%; Score 179; DB 17; Length 37;
Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 DVDATATRGSAASRPTERRAPARSASRRPRVE 301
DB 2 DVDATATRGSAASRPTERRAPARSASRRPRVE 37

RESULT 5
US-09-415-795-27
; Sequence 27, Application US/09415795
; GENERAL INFORMATION:
; APPLICANT: Zhou, Pengbo
; APPLICANT: Howley, Peter M.
; TITLE OF INVENTION: TARGETED PROTEOLYSIS BY RECRUITMENT TO UBIQUITIN
; FILE REFERENCE: HMV-043.01
; CURRENT APPLICATION NUMBER: US/09/415,795
; CURRENT FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VP22 (C-terminal domain)
; US-09-415-795-27

Query Match
Best Local Similarity 100.0%; Score 179; DB 18; Length 37;
Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 266 DVDAATATGRSAASRPTERRAPARASRRPRPVE 301
Db 2 DVDAATATGRSAASRPTERRAPARASRRPRPVE 37

RESULT 6
US-09-718-233-16
Sequence 16, Application US/09718233
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
Lampheire, Lou
Beach, David H.
TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION AND RELATED THERETO
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/718.233
FILING DATE: 21-Nov-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-069.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-718-233-16

Query Match 11.5%; Score 179; DB 21; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 266 DVDAATATGRSAASRPTERRAPARASRRPRPVE 301
Db 2 DVDAATATGRSAASRPTERRAPARASRRPRPVE 37

RESULT 7
US-09-011-073-2
Sequence 2, Application US/09011073
GENERAL INFORMATION:
APPLICANT: O'Hare et al.
TITLE OF INVENTION: TRANSPORT PROTEINS AND THEIR USES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
Winston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon

COUNTRY: United States of America
ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 7.0 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011.073
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01831
FILING DATE: JULY 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Ealp, David J.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 5759-49294/DJE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 34
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-011-073-2

Query Match 10.8%; Score 169; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 268 DATATGRSAASRPTERRAPARASRRPRPVE 301
Db 1 DATATGRSAASRPTERRAPARASRRPRPVE 34

RESULT 8
US-09-229-486-2
Sequence 2, Application US/09229486
GENERAL INFORMATION:
APPLICANT: O'Hare et al.
TITLE OF INVENTION: Transport proteins and their uses
FILE REFERENCE: 5146
CURRENT APPLICATION NUMBER: US/09/229.486
EARLIER FILING DATE: 1999-01-13
EARLIER APPLICATION NUMBER: PCT/GB96/01831
EARLIER FILING DATE: 1996-07-25
EARLIER APPLICATION NUMBER: GB 9601570.6
EARLIER FILING DATE: 1996-01-26
EARLIER APPLICATION NUMBER: GB 9515568.5
EARLIER FILING DATE: 1995-07-28
EARLIER APPLICATION NUMBER: US 09/011.073
EARLIER FILING DATE: 1998-01-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 34
TYPE: PRT
ORGANISM: herpes simplex virus type 1
US-09-229-486-2

Query Match 10.8%; Score 169; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 268 DATATGRSAASRPTERRAPARASRRPRPVE 301
Db 1 DATATGRSAASRPTERRAPARASRRPRPVE 34

RESULT 9
US-09-773-430-2
; Sequence 2, Application US/09773430
; GENERAL INFORMATION:
; APPLICANT: O'Hare et al.
; TITLE OF INVENTION: TRANSPORT PROTEINS AND THEIR USES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; Whinston, LLP
; STREET: One World Trade Center
; 121 S.W. Salmon Street
; Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 7.0 & ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/773,430
; FILING DATE: 31-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/011,073
; FILING DATE: 1998-07-26
; ATTORNEY/AGENT INFORMATION:
; NAME: Earp, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 5759-49294/DUE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-773-430-2

Query Match 10.8%; Score 169; DB 21; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 268 DAATATGRSASRPTERRPAPARSRRPRPYE 301
|||||
Db 1 DAATATGRSASRPTERRPAPARSRRPRPYE 34

RESULT 10
US-10-083-889-19
; Sequence 19, Application US/10083889
; GENERAL INFORMATION:
; APPLICANT: Zahner, Joseph E.
; TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
; FILE REFERENCE: 16850-7331
; CURRENT APPLICATION NUMBER: US/10/083,889
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/271,798
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 19
; LENGTH: 34
; TYPE: PRT
; ORGANISM: mammal

US-10-083-889-19

Query Match 10.8%; Score 169; DB 24; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 268 DAATATGRSASRPTERRPAPARSRRPRPYE 301
|||||
Db 1 DAATATGRSASRPTERRPAPARSRRPRPYE 34

RESULT 11
US-09-780-070-39
; Sequence 39, Application US/09780070
; GENERAL INFORMATION:
; APPLICANT: Burke, James
; APPLICANT: Stillwater, Warren
; APPLICANT: Nagai, Yoshitaka
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPE
; FILE REFERENCE: 5405.242
; CURRENT APPLICATION NUMBER: US/09/780,070
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 34
; TYPE: PRT
; ORGANISM: herpes simplex virus type 1
US-09-780-070-39

Query Match 10.6%; Score 166; DB 21; Length 34;
Best Local Similarity 97.1%; Pred. No. 0.00019;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 268 DAATATGRSASRPTERRPAPARSRRPRPYD 301
|||||
Db 1 DAATATGRSASRPTERRPAPARSRRPRPYD 34

RESULT 12
US-09-617-682A-15494
; Sequence 15494, Application US/09617682A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
; FILE REFERENCE: 2750-1063P
; CURRENT APPLICATION NUMBER: US/09/617,682A
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 16871
; SEQ ID NO 15494
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..48
; OTHER INFORMATION: xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..48
; OTHER INFORMATION: Ceres Seq. ID 1424260
US-09-617-682A-15494

Query Match 4.7%; Score 73; DB 20; Length 48;
Best Local Similarity 45.0%; Pred. No. 8.6e+02;
Matches 18; Conservative 5; Mismatches 15; Indels 2; Gaps 2;

Oy 96 PPARAPPAGSGAGRTPTTAPRAPRTQVATKAPAP 135
DB 11 PGSA-SPSSPGSTGSARPTTASTAP-PATTTTNSPADP 48

RESULT 13

US-10-029-386-31973
Sequence 31973, Application US/10029386
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Hank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
FILE REFERENCE: AECOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31973
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL137784.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.92
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
US-10-029-386-31973

Query Match 4.5%; Score 69.5; DB 24; Length 43;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 4; Mismatches 8; Indels 3; Gaps 1;

Oy 272 ATRGSAASRTPRRPARP---SASRP 298
DB 4 AVRGRASSARPLPRPPRRPQASGSPRR 33

RESULT 14

US-09-880-578-32
Sequence 32, Application US/09880578
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Presnell, Scott R.
APPLICANT: Jelmeberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Foster, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehnert, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,578
FILING DATE: 13-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-880-578-32

Query Match 4.4%; Score 68.5; DB 22; Length 48;
Best Local Similarity 37.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 5; Mismatches 14; Indels 15; Gaps 3;

Oy 98 PARAPPAGSGAGRTPTTAPRAPRTQVATKAPAPAEETTRGRKSAOPESA 151
DB 9 PPRAPPPS-----RSP---BRAPCS-----AGPMAPAGMPACGRCPAQA 47

RESULT 15

US-09-708-427-46419
Sequence 46419, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46419
LENGTH: 47
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..47
OTHER INFORMATION: xaa is any amino acid
NAME/KEY: misc.feature
LOCATION: 1..47
OTHER INFORMATION: Ceres Seq. ID 1852321
US-09-708-427-46419

Query Match 4.3%; Score 67.5; DB 21; Length 47;
Best Local Similarity 39.5%; Pred. No. 2e+03;
Matches 17; Conservative 4; Mismatches 15; Indels 7; Gaps 2;

Oy 79 PEVPRTRRVSGAVLSGPP-ARAPPAGSGAGTPTTAR 120
DB 10 PPLPSKRPAPAGIPSTPGSRLAAPL-----KKPTLADR 46

Search completed: August 28, 2002, 12:31:12
Job time: 210 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:26:21 ; Search time 13.08 Seconds
(without alignments)
562.087 Million cell updates/sec

Title: US-09-522-278B-12

Perfect score: 1561

Sequence: 1 MTSRRSYKSGPREYPRDEYE.....PTERRPARASRRPRPE 301

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 164183

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*

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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PC1US.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	169	10.8	34	US-09-011-073A-2	Sequence 2, Appl1
2	166	10.6	32	US-09-230-421-14	Sequence 14, Appl1
3	117	7.5	20	US-09-230-421-6	Sequence 6, Appl1
4	108	6.9	20	US-09-230-421-5	Sequence 5, Appl1
5	106	6.8	20	US-09-230-421-9	Sequence 9, Appl1
6	103	6.6	20	US-09-230-421-7	Sequence 7, Appl1
7	103	6.6	20	US-09-230-421-8	Sequence 8, Appl1
8	100	6.4	20	US-09-230-421-11	Sequence 11, Appl1
9	99	6.3	20	US-09-230-421-10	Sequence 10, Appl1
10	89	5.7	20	US-09-230-421-12	Sequence 12, Appl1
11	73	4.7	20	US-09-071-224-32	Sequence 4, Appl1
12	68.5	4.4	48	US-09-071-224-32	Sequence 32, Appl1
13	65.5	4.2	48	5171685-7	Patent No. 5171685
14	65.5	4.2	48	5518916-7	Patent No. 5518916
15	64.5	4.1	42	US-08-476-866-23	Sequence 23, Appl1
16	62	4.0	45	US-08-676-279-56	Sequence 56, Appl1
17	59	3.8	35	US-09-001-984C-11	Sequence 11, Appl1
18	58	3.7	35	US-09-001-984C-42	Sequence 42, Appl1
19	58	3.7	48	US-07-609-716-106	Sequence 106, App
20	58	3.7	48	US-08-475-411A-106	Sequence 106, App
21	58	3.7	48	US-08-478-029A-106	Sequence 106, App
22	55.5	3.6	33	US-09-071-224-33	Sequence 33, Appl1
23	55	3.5	33	US-08-237-716-11	Sequence 11, Appl1
24	54.5	3.5	46	US-08-483-533-30	Sequence 30, Appl1
25	54.5	3.5	46	US-09-283-471A-30	Sequence 30, Appl1
26	53	3.4	48	US-09-314-268-164	Sequence 164, App
27	52	3.3	20	US-09-010-928B-9	Sequence 9, Appl1

28	52	3.3	34	1	US-08-433-854-12	Sequence 12, Appl1
29	52	3.3	34	1	US-08-174-745A-12	Sequence 12, Appl1
30	52	3.3	34	2	US-08-195-947-12	Sequence 12, Appl1
31	52	3.3	34	2	US-08-433-885-12	Sequence 12, Appl1
32	52	3.3	34	2	US-08-433-908B-12	Sequence 12, Appl1
33	52	3.3	34	4	US-08-410-614-12	Sequence 12, Appl1
34	51.5	3.3	40	4	US-09-314-268-165	Sequence 165, App
35	51.5	3.3	41	1	US-07-609-716-57	Sequence 57, Appl1
36	51.5	3.3	41	1	US-08-642-255-27	Sequence 27, Appl1
37	51.5	3.3	41	4	US-08-475-411A-57	Sequence 57, Appl1
38	51.5	3.3	41	4	US-08-478-029A-57	Sequence 57, Appl1
39	51	3.3	24	1	US-08-031-148-5	Sequence 5, Appl1
40	51	3.3	24	2	US-08-306-078-2	Sequence 2, Appl1
41	51	3.3	24	3	US-08-415-838-5	Sequence 5, Appl1
42	51	3.3	40	4	US-08-672-213-29	Sequence 29, Appl1
43	50.5	3.2	36	1	US-07-972-032-67	Sequence 67, Appl1
44	50.5	3.2	36	1	US-08-642-255-79	Sequence 79, Appl1
45	50.5	3.2	40	1	US-08-099-354-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-011-073A-2
Sequence 2 Application US/09011073A
Patent No. 6184038
GENERAL INFORMATION:
APPLICANT: O-Chate et al.
TITLE OF INVENTION: TRANSPORT PROTEINS AND THEIR USES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESS: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
CITY: Suite 1600
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 7.0 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011.073A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/G896/01831
FILING DATE: JULY 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Earp, David J.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 5759-49294/DJE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 34
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-011-073A-2

Query Match 10.8%; Score 169; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 34; Conservative 0; Mismatches 0; Gaps 0;

```
OY 268 DAATATGRGSASRPTERRAPARASRRPRPYE 301
      |||||||
DB 1 DAATATGRGSASRPTERRAPARASRRPRPYE 34

RESULT 2
US-09-230-421-14
; Sequence 14, Application US/09230421.
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
; OTHER INFORMATION: SEQUENCE
US-09-230-421-14

Query Match 10.6%; Score 166; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 190 TPRVAGFNKRVCFAVGRLLAAMHARMAAVQLW 221
      |||||||
DB 1 TPRVAGFNKRVCFAVGRLLAAMHARMAAVQLW 32

RESULT 3
US-09-230-421-6
; Sequence 6, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
; OTHER INFORMATION: SEQUENCE
US-09-230-421-6

Query Match 7.5%; Score 117; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 178 ESTAPPNPDAWMTPRVAGFN 197
      |||||||
DB 1 ESTAPPNPDAWMTPRVAGFN 20

RESULT 4
US-09-230-421-5
; Sequence 5, Application US/09230421
; Patent No. 6200577
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; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
; OTHER INFORMATION: SEQUENCE
US-09-230-421-5

Query Match 6.9%; Score 108; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 KTPAGGLARKLHSTAPPNP 185
      |||||||
DB 1 KTPAGGLARKLHSTAPPNP 20

RESULT 5
US-09-230-421-9
; Sequence 9, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
; OTHER INFORMATION: SEQUENCE
US-09-230-421-9

Query Match 6.8%; Score 106; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 214 RMAAVQLMDMSRPRTDEDLN 233
      |||||||
DB 1 RMAAVQLMDMSRPRTDEDLN 20

RESULT 6
US-09-230-421-7
; Sequence 7, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
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; SEQ ID NO 7
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
US-09-230-421-7

Query Match 6.6%; Score 103; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 190 TPVAGFNKRVFCAVGR1A 209
Db 1 TPVAGFNKRVFCAVGR1A 20

RESULT 7
US-09-230-421-8
; Sequence 8, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
US-09-230-421-8

Query Match 6.6%; Score 103; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAVGR1AAMHARMAVQLM 221
Db 1 CAVGR1AAMHARMAVQLM 20

RESULT 8
US-09-230-421-11
; Sequence 11, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
US-09-230-421-11

Query Match 6.4%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 ITTIRVTCGKRLQORANE 257
Db 1 ITTIRVTCGKRLQORANE 20

RESULT 9
US-09-230-421-10
; Sequence 10, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
US-09-230-421-10

Query Match 6.3%; Score 99; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 PRDEDLNELLGITTRIVTV 245
Db 1 PRDEDLNELLGITTRIVTV 20

RESULT 10
US-09-230-421-12
; Sequence 12, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
US-09-230-421-12

Query Match 5.7%; Score 89; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 NILQANELVNDPVQDV 267
Db 1 NILQANELVNDPVQDV 18

RESULT 11
US-09-230-421-4
; Sequence 4, Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
; OTHER INFORMATION: SEQUENCE
US-09-230-421-4

Query Match 4.7%; Score 73; DB 4; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.2;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 158 APTAPTRSKTPAOGLA 173
| | | | | | | | | | | | | | | | | | | | | |
DB 5 APTAPTRSKTPAOGLA 20

RESULT 12
US-09-071-224-32
; Sequence 32, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, SI
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6677
; TELEFAX: 206-442-6678

TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-224-32

Query Match 4.4%; Score 68.5; DB 4; Length 48;
Best Local Similarity 37.0%; Pred. No. 16;
Matches 20; Conservative 5; Mismatches 14; Indels 15; Gaps 3;

OY 98 PARAPPPAGSGAGRTPTTAPAPRTQVATKAPAPAEETTRGKSAQESA 151
| | | | | | | | | | | | | | | | | | | | | |
DB 9 PRAPPPPPS-----RSP---PRAPGS-----AGPMAGPMAGRGRAQSA 47

RESULT 13
5171685-7
; Patent No. 5171685
; APPLICANT: MCELMAN, TERRY F.; HINES, STEPHEN A.; MCGUIRE,
; TRAVIS C.; PALMER, GUY H.; JASMER, DOUGLAS P.; REDUKER, DAVID W.
; GOFF, WILL L.; PERRYMAN, LANCE E.; DAVIS, WILLIAM C.
; TITLE OF INVENTION: CLONING OF THE BABESIA BOVIS 60 KD ANTIGEN
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/504,461
; FILING DATE: 04-APR-1990
; SEQ ID NO: 7
; LENGTH: 48
5171685-7

Query Match 4.2%; Score 65.5; DB 6; Length 48;
Best Local Similarity 35.1%; Pred. No. 30;
Matches 20; Conservative 5; Mismatches 21; Indels 11; Gaps 2;

OY 132 PAAPAEETTRGKSAQESALPDAPASTAPTRSKTPAOGLAARKLHFTAPPPDPAP 188
| | | | | | | | | | | | | | | | | | | | | |
DB 1 PPRP-AETQOTQDSAPSTPAPSPPPQRAET-----QQTQDSTAPGTPAP 46

RESULT 14
5518916-7
; Patent No. 5518916
; APPLICANT: MCELMAN, TERRY F.; MCGUIRE, TRAVIS C.; JASMER,
; DOUGLAS P.; REDUKER, DAVID W.; GOFF, WILL L.; STILLNER, DAVID
; TITLE OF INVENTION: CLONED BABESIA DNA
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,480
; FILING DATE: 21-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 989,616
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: 504,461
; FILING DATE: 04-APR-1990
; APPLICATION NUMBER: 333,155
; FILING DATE: 04-APR-1989
; SEQ ID NO: 7
; LENGTH: 48
5518916-7

Query Match 4.2%; Score 65.5; DB 6; Length 48;
Best Local Similarity 35.1%; Pred. No. 30;
Matches 20; Conservative 5; Mismatches 21; Indels 11; Gaps 2;

OY 132 PAAPAEETTRGKSAQESALPDAPASTAPTRSKTPAOGLAARKLHFTAPPPDPAP 188
| | | | | | | | | | | | | | | | | | | | | |

Db 1 PORP-AETQOTODSAPSTPAAPSPQRPAPET-----QOTQDSTAPCTPAAP 46

RESULT 15

US-08-476-866-23

; Sequence 23, Application US/08476866
; Patent No. 5994339

GENERAL INFORMATION:

APPLICANT: CRAPO, JAMES D.

APPLICANT: FRIDOVICH, IRWIN

APPLICANT: OURI, TIM

APPLICANT: DAY, BRIAN J.

APPLICANT: FOLZ, RODNEY J.

APPLICANT: FREEMAN, BRUCE A.

TITLE OF INVENTION: SUPEROXIDE DISMUTASE AND MIMETICS THEREOF

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,866

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/322,766

FILING DATE: 13-OCT-1994

APPLICATION NUMBER: US 08/136,207

FILING DATE: 15-OCT-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-74

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-476-866-23

Query Match 4.1%; Score 64.5; DB 2; Length 42;

Best Local Similarity 36.6%; Pred. No. 31;

Matches 15; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

OY 103 PPPAGSGGAGRTTAPRAP-RTQRYATKAPAPAAETTRG 142

Db 1 PASSSSGSIRPAPSSSTPSPMARASRSPRIAPAPSTCTSSG 41

Search completed: August 28, 2002, 12:28:53
Job time: 152 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:24:01 ; Search time 13.42 Seconds

(without alignments)
868,449 Million cell updates/sec

Title: US-09-522-278b-12

Perfect score: 1561

Sequence: 1 MTSRSRVKSGPREVPRDEYE.....PTERRPARASAPRRPVE 301

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1561	100.0	301	1	UL49_HSV11
2	303	19.4	304	1	UL49_HSV11
3	271.5	17.4	258	1	UL49_HSV11
4	270.5	17.3	290	1	UL49_HSV11
5	225.5	14.4	302	1	UL49_HSV11
6	166	10.6	1461	1	UL49_HSV11
7	161.5	10.3	660	1	UL49_HSV11
8	153.5	9.8	1446	1	UL49_HSV11
9	142.5	9.1	263	1	UL49_HSV11
10	138	8.6	806	1	UL49_HSV11
11	135	8.6	261	1	UL49_HSV11
12	134.5	8.6	3149	1	UL49_HSV11
13	133.5	8.6	852	1	UL49_HSV11
14	133	8.5	1509	1	UL49_HSV11
15	130.5	8.4	591	1	UL49_HSV11
16	130	8.3	857	1	UL49_HSV11
17	128.5	8.2	731	1	UL49_HSV11
18	127.5	8.2	607	1	UL49_HSV11
19	127	8.1	3164	1	UL49_HSV11
20	126.5	8.1	320	1	UL49_HSV11
21	126.5	8.1	561	1	UL49_HSV11
22	126.5	8.1	628	1	UL49_HSV11
23	126.5	8.1	1298	1	UL49_HSV11
24	125.5	8.0	252	1	UL49_HSV11
25	125	8.0	239	1	UL49_HSV11
26	124.5	8.0	217	1	UL49_HSV11
27	124.5	8.0	226	1	UL49_HSV11
28	124	7.9	1163	1	UL49_HSV11
29	123.5	7.8	1001	1	UL49_HSV11
30	122.5	7.8	1217	1	UL49_HSV11
31	122	7.8	428	1	UL49_HSV11
32	122	7.8	704	1	UL49_HSV11
33	122	7.8	1575	1	UL49_HSV11

34	121.5	7.8	924	1	104K_THEPA
35	121.5	7.8	1083	1	T2D3_HUMAN
36	120.5	7.7	699	1	NP14_HUMAN
37	120	7.7	761	1	TIE2_BRARE
38	120	7.7	1418	1	CA12_HUMAN
39	119.5	7.7	309	1	HCX4_CHICK
40	119	7.6	825	1	ICP0_HSV11
41	118	7.6	1459	1	CA12_MOUSE
42	117	7.5	314	1	PKXB_MOUSE
43	117	7.5	314	1	PKXB_MOUSE
44	117	7.5	431	1	UL61_HCVMA
45	117	7.5	512	1	IE63_HSV11

ALIGNMENTS

RESULT 1	UL49_HSV11	STANDARD:	PRT:	301 AA.
ID	UL49_HSV11			
AC	P10233:			
DT	01-MAR-1989 (rel. 10, Created)			
DT	01-MAR-1989 (rel. 10, Last sequence update)			
DT	01-DEC-1992 (rel. 24, Last annotation update)			
DE	Tegument protein UL49.			
GN	UL49.			
OS	Herpes simplex virus (type 1 / strain 17).			
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
OC	Alphaherpesvirinae; Simplexvirus.			
OX	NCBI_TaxID=10299;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RX	MEDLINE=86274327; PubMed=2639594;			
RA	McGeoch D.J., Dalrymple M.A., Davidson A.J., Dolan A., Frame M.C.,			
RT	McNab D., Perry L.J., Scott J.E., Taylor P.			
RT	"The complete DNA sequence of the long unique region in the genome of			
RT	herpes simplex virus type 1."			
RL	J. Gen. Virol. 69:1531-1574(1988).			
CC	1. SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL49,			
CC	EHV-1 11, AND VZV 9.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: D10879; BAA01695.1; -			
DR	EMBL: X14112; CAA32299.1; -			
DR	PIR: D30089; WMBE9.			
SO	SEQUENCE 301 AA; 32254 MW; 6E9539C2AE13E29 CRC64;			
Query Match	100.0%; Score 1561; DB 1; Length 301;			
Best Local Similarity	100.0%; Pred. No. 3e-82;			
Matches 301; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 MTSRSRVKSGPREVPRDEYEEDLYTPSSGMASSPDPSTSRGALQTRRORGEVFFVOY 60			P15711 thelleria p
DB	1 MTSRSRVKSGPREVPRDEYEEDLYTPSSGMASSPDPSTSRGALQTRRORGEVFFVOY 60			000268 homo sapien
OY	61 DESDVALYGGSSSEDEHPEVPRTRRPVSGAVLSCGPAPAPPPPGSGAGRTPTTAPR 120			014978 homo sapien
DB	61 DESDVALYGGSSSEDEHPEVPRTRRPVSGAVLSCGPAPAPPPPGSGAGRTPTTAPR 120			013166 brachydanio
OY	121 APTQVAVAKKAAPAAETTRRKRKSNQPSAALPPAPATATRTSTPAQGLARKLHFT 180			P02458 homo sapien
DB	121 APTQVAVAKKAAPAAETTRRKRKSNQPSAALPPAPATATRTSTPAQGLARKLHFT 180			P17277 gallus galli
OY	181 APPNDAPPTPVAGFNKRVFCAAVGRLAMHARMAAVALMDMSRPTDEEDNELGLTTF 240			P28284 herpes simp
DB	181 APPNDAPPTPVAGFNKRVFCAAVGRLAMHARMAAVALMDMSRPTDEEDNELGLTTF 240			P28481 mus musculu
				O99453 homo sapien
				O35690 mus musculu
				P16818 human cytom
				P10238 herpes simp

```

Db      181 APPNDADWTPVSAFENKRVCEACAAVGRLAAMHARMAAVQJMDMSRPRTDEDINELLGITP   240
Oy      241 IRRVYCEBKNNLQRANLEYNPVDVDDVAATPTRGRSAASRTERPRAPARSARRPV    300
Db      241 IRRVYCEBKNNLQRANLEYNPVDVDDVAATPTRGRSAASRTERPRAPARSARRPV    300
Oy      301 E 301
Db      301 E 301

RESULT          2
UL49_HSVEB     STANDARD:             PRT:       304 AA.
ID_UL49_HSVEB
AC_P28960:
DT_01-DEC-1992 (Rel. 24, Created)
DT_01-DEC-1992 (Rel. 24, Last sequence update)
DT_01-DEC-1992 (Rel. 24, Last annotation update)
DE_Tegument protein (Gene 11 protein).
OS_Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
OC_Viruses; dsDNA Viruses, no RNA stage; Herpesviridae;
OC_Alphaherpesvirinae; Varicelloviruses.
OX_NCB1_TaxID=31520:
RN [1]
RX_SEQUENCE FROM N.A. MEDLINE=92295566; PubMed=1318606;
RX_Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1.";
RL_Virology 189:304-316(1992).
CC_-I- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL49,
CC_EHV-1 11, AND VAV 9.
CC-----
CC_This SWISS-PROT entry is copyright. It is produced through a collaboratior
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CC_or send an email to license@isb-slb.ch).
CC-----
DR_EMBL: M86664; AAB02446.1; -.
DR_PIN: C36796; WZBEA9.
SQ_SEQUENCE 304 AA; 33240 MW; 937CE27366E79879 CRC64;
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	Query Match	19.4%	Score 303;	DB 1;	Length 304;	
	Best Local Similarity	32.4%;	Pred. No. 5.2e-11;			
	Matches	93;	Conservative	30;	Mismatches 96;	Indels 68; Gaps 11.
OY	DLYVPPSSGMASPDSPDPDPSRRGALQTSRSGEVRFO-----YDSDDALYGSSS	73				
	: :	:	:	:	:	:
Db	DLYES-----ASPNDKXYTRRG-WSTAHHYDSEHITYTCGDGYDCETSLIG----	108				
	:	:	:	:	:	:
OY	EDDEHEVPRTRRPVAVLSGPG--PARAPPPAGSGCAGRPTTAPRAERTORVATK	130				
	: : :	:	:	:	:	:
Db	109 -----GKLSTNSGRSQSPAKAQPPRGAA----PEPRVYRTPPTTAAT-	149				
	:	:	:	:	:	:
OY	131 APAARAEETTRCKRSQAOPESALPPOAPASTARTSKTPNOGLARKLHFESTAPPNPDAPT	190				
	: :	:	:	:	:	:
Db	150 -----STTPROQOCAPQRASP-----VNSIKSGCLA---FSGTEKTPKSOMY	191				
	: :	:	:	:	:	:
OY	191 PRVAGFNRFCCAAGRLAAMHAAMAVALWMSRPRTDEDENELGITITRVTCCEGN	250				
	:	:	:	:	:	:
Db	192 GATHLEFNKNVFCAAYSRVAAMHASDASLMDLNPKTKTEDLDRLFKAATITLVCEGAO	251				
	:	:	:	:	:	:
OY	251 LLQARANLVNPDVODVDATAATTRGSASAAPTERTPRAPARSASRPR	297				
	: :	:	:	:	:	:
Db	252 LLEVANSTMTE-----STPGVYAAGNGVDRRP-RFASRRR	286				
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ID	UL49_HSVBC	STANDARD:	PRT:	258 AA.
AC	P30022:			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Tegument protein UL49 homolog.			
OS	Bovine herpesvirus type 1 (strain Cooper).			
CC	Virusess; dsDNA viruses; no RNA stage; Herpesviridae;			
OC	Alphaherpesvirinae; Varicellovirus.			
OX	NCBL_TaxID=10323;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Schwayer M., Styger D., Vogt B., Lowery D.E., Simard C.,			
RA	Lapossiere S., Misra V., Vlcek C., Paces V.;			
RL	Submitted (SEP-1995) to the EMBL/Genbank/DDBJ databases.			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=95264482; Pubmed=7745736;			
RX	Liang X., Chow B., Li Y., Rago C., Yoo D., Attah-Poku S.,			
RA	Bablik L.A.;			
RT	"Characterization of bovine herpesvirus 1 UL49 homolog gene and			
RT	product: Bovine herpesvirus 1 UL49 homolog is dispensable for virus			
RT	growth.";			
RL	J. Virol. 69:3863-3867(1995).			
RN	[3]			
RP	SEQUENCE OF 1-95 FROM N.A.			
RA	MEDLINE=9303938; Pubmed=8391186;			
RX	Liang X., Tang M., Manns B., Bablik L.A., Zamb T.J.;			
RT	"Identification and deletion mutagenesis of the bovine herpesvirus 1			
RT	dutpase gene and a gene homologous to herpes simplex virus UL49.5.";			
RL	Virology 195:42-50(1993).			
RN	[4]			
RP	SEQUENCE OF 64-258 FROM N.A.			
RA	MEDLINE=93012995; Pubmed=1327963;			
RT	Carpenter D.E., Mistra V.;			
RT	"Sequences of the bovine herpesvirus 1 homologue of herpes simplex			
RT	virus type-1 alpha-trans-inducing factor (UL48).";			
RL	Gene 119:259-263(1992).			
CC	-I- SIMILIARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL49,			
CC	BEHV-1.II. AND VZV 9.			
CC				
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CC	or send an email to license@isb-sib.ch).			
CC				
DR	EMBL; Z54206; CAAG90920.1; -			
DR	EMBL; U21137; AAA85715.1; -			
DR	EMBL; Z11610; -; NOT_ANNOTATED_CDS.			
PT	PIR; S24228; S24228.			
FT	DOMAIN 61 91 ALA-RICH.			
QO	SEQUENCE 258 AA; 26864 MW; 78C5567442EBA161 CRC64;			

Query Match	17.4%	Score 271.5;	DB 1;	Length 256;
Best Local Similarity	31.2%;	Pred. No. 2.7e-09;		
Matches 81;	Conservative 25;	Mismatches 109;	Indels 45;	Gaps 8;

QY	61	DESDY-----	ALYGGSSSEDDHEPEVPRTRRYPGAVLSCGPD-----	-A	99
					:
Db	10	DEDEYEEDLWRENSLYDYESGSDHYELR-----	AATSGPEESGRASRVACAS		62
QY	100	RAPPPAGSG-----	GAGRT---PTTAPRAPRTQGVATKAPAAPA-----	AETTRGRKSA	146
Db	63	AAAVQAPARGDRRAAAGTTVAAPAAAVARRSSSRASSRPRAADPVLRLPATRGSSGC			122
QY	147	QPE\$ALPDAPASNAPTFTSKTTPAGGLAKLTF\$TAAPRPDPAAPPRVAGFKKRP\$CAV\$A			206
Db	123	AGAAVAVG\$-PRPRAPPGCANAVASG\$-RPL\$FSAAPKTPKAPWCGCPHTHAYRRTTCEVNA			178

[illegible]

RESULT	4
UL49_HSVEA4	STANDARD; PRT; 290 AA.
AC	0000039;
DT	01-DEC-1992 (Rel. 24, Created)
DT	01-DEC-1992 (Rel. 24, Last sequence update)
DT	01-DEC-1992 (Rel. 24, Last annotation update)
DE	Tegument protein (gene 11 protein).
GN	11 OR B4.
OS	Equine herpesvirus type 4 (strain 1942) (EHV-4) (Equine herpesvirus type 1 subtype 2).
OS	viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC	Alphaherpesvirinae; Varicellovirus.
OX	NCBI_TaxID=10333;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91202570: PubMed=1850013:
RA	Whittaker G.R., Riggio M.P., Halliburton I.W., Killington R.A.,
RA	Allen G.P., Merditt D.M.:
RT	"Antigenic and protein sequence homology between VP13/14, a herpes simplex virus type 1 tegument protein, and gp10, a glycoprotein of equine herpesvirus 1 and 4.";
RT	J. Virol. 65:2330-2336(1991).
CC	-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL49, EHV-1 11, AND VZV 9.
CC	-----
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CC	or send an email to license@isb-sib.ch .
CC	-----
DR	EMBL: X17684; CAA35674.1; -
DR	PIR: S36706; S36706.
DR	SEQUENCE 290 AA; 31461 MW; BD57CE14436295FC CRC64;

Query Match	17.3%	Score 270.5	DB:1	Length 290
Best Local Similarity	34.4%	Pos. No. 3.4e-09		
Matches 83	Conservative 18	Mismatches 77	Indels 67	Gaps 11
OY	60	YDES DYAL YGSSSDEDEHPEVPTRRPESGAVLSGPG---PARAPPPAGSGAGRPPT	116	
		: :		: :
Db	84	YDACEYSLVSG-----GKLSHSGRLSPTKTTPHPK---SAGVTP	120	
OY	117	TAPAPPRQVATKAPAPAAETTRGRKSAQPESSALCLDPASTAPPTSKTPAGCL--AR	174	
		: :		: :
Db	121	-----PQR-----PARPAT-----RAAP--SATPTQPCVAKQRTSPGVNSIKSGK	161	
OY	175	KLAFSTAPPNPDAPWTPRVAGFNKRKFVCCAAGRLAAHMAHARAAYOLVUMSRRPTDENE	234	
		: :		: :
Db	162	SLAFSCPRKTPKTPMYGATHLEFNKKVFCAAVSRVAALHAASALMDLPDKTNMEDLR	221	
OY	235	LGITTTTAVTCECKNLLORANGLVNPVODVDAATTRGRS---AASRPTERPAPA	290	
		: :		: :
Db	222	FLKAAAIRILVCEGSKLEMAN-----ATMERSPDGAANAVALIGYDRP-	265	
OY	291	RSASRPR	297	
		: :		: :
Db	266	RLASRRR	272	

```

RESULT 5
ID UL49_VZVD STANDARD: PRT: 302 AA.
AC P09272;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Tegument protein (Gene 9 protein).
CN 9.
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OX Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=10338;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86306657; PubMed=3018124;
RA Davison A.J., Scott J.E.;
RL "The complete DNA sequence of varicella-zoster virus.";
CC J. Gen. Virol. 67:1759-1816(1986).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL49,
CC EHV-1 11, AND VZV 9.
CC -----
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CC -----
DR EMBL; X04370; CAA27892.1; -
PIR: I27212; WZBE9.
SEQUENCE 302 AA; 32846 MW; 6557EB44CAE76BF2 CRC64;

```

	Query Match	14.4%:	Score 225.5:	DB 1:	Length 302:	
	Best Local Similarity	26.2%:	Pred. No. 1.3e-06:			
	Matches 89:	Conservative 27:	Mismatches 107:	Indels 117:	Gaps 10:	
OY	2 TSRSRVKSGP-----REVRDVEEDLYLPTSSGMA SPDP TSRRGALQ 46	: :		:	:	
Db	29 TARSRVVVGPDDSDSLGITTVADSDPSRYALLDFENHKTTTPRVHPNDSS----- 82	: :		:	:	
OY	47 TRSRORGEVFVQYDESYALYGSSSEDEHEVPRTRRP-----VSGAIVSGCPBA 99	: :		:	:	
Db	83 -----GSEDDFEDIDEVAAAFREARLRHETVEDAVYENPLSV 119	: :		:	:	
OY	100 RAPPPAGSGAGRPTTAPRAPRTRQVATXAKRARAPAEATTGRKSADPEASALDAPAS 159	: :		:	:	
Db	120 EKP-----SRSETKAA-----VKPK--LEDSP-k 141	: :		:	:	
OY	160 TAPTSTKTPAOGLARLKLFSTARPNDAFWTPRVVGFNGKRVFCAAVGRLAAMHARMAAVO 219	: :		:	:	
Db	142 RAPPAGAIASG--RPISFTSAPRKATGTSWCGPRPSYNKNRVPCSAVIRVAAMOQAADA 199	: :		:	:	
OY	220 LMDMSRPTDEDLNLLEITITRIYVCGSKNLLQANE----- 257	: :		:	:	
Db	200 AMNSNPNNMELDLGLCAVIRIVHGLNIQLQANEDLGEGASYSKRGHNRTGTGLQ 259	: :		:	:	
OY	258 -LVNPDVVDVDAATATGRGSAA SPERPAP ARSR 295	: :		:	:	
Db	260 GGMGNRPYAYQRKPKSRDTQTGTGRITNRSR--ARSA SR 297	: :		:	:	
RESULT	6					
IE18_PRIVIF	IE18_PRIVIF	STANDARD:	PRT:	1461 AA.		
AC	P1675:					
DT	01-OCT-1989 (Rel. 12, Created)					
DT	01-APR-1990 (Rel. 14, Last sequence update)					
DT	01-FEB-1994 (Rel. 28, Last annotation update)					
DN	Immediate-early protein IE180.					
IE	IE.					

RESULT	ID	PRVKA	STANDARD	PRT	1446 AA
IE18	IE18_PRVKA				
AC	P33479				
DT	01-FEB-1994	(Rel. 28, Created)			
DT	01-FEB-1994	(Rel. 28, Last sequence update)			
DT	01-FEB-1994	(Rel. 28, Last annotation update)			
DE	Immediate-early protein IE180.				
GN	IE.				
OS	Pseudorabies virus (strain Kaplan) (PRV).				
OC	Viruses: dsDNA viruses, no RNA stage: Herpesviridae;				
OC	Alphaherpesvirinae: Varicelloviruses.				
OX	NCBI_TaxID=33703;				
RM	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91021039; PubMed=2171211;				
RA	Vleck C., Kozmik Z., Paces V., Schirm S., Schwytzer M.;				
RT	"Pseudorabies virus immediate-early gene overlaps with an oppositely				
RT	oriented open reading frame: characterization of their promoter and				
RT	enhancer regions.";				
RL	Virology 179:365-377(1990).				
CC	-1- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE				
CC	OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING				
CC	OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.				
CC	-1- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.				
CC	-1- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF				
CC	PHOSPHORYLATION.				
CC	-1- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.				
CC	-----				
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CC	-----				
DR	EMBL; M34651; AAA47470.1; -.				
DR	PIR; A45344; A45344.				
KW	Early Protein; Transcription regulation; Trans-acting factor;				
KW	DNA-binding; Phosphorylation; Nuclear protein.				
FT	DOMAIN 347 354 POLY-SER.				
FT	DOMAIN 379 397 POLY-SER.				
SO	SEQUENCE 1446 AA; 148640 MW; 81F3A3DE3DDA068 CRC64;				
Query Match 9.8%; Pred. 153.5; DB 1; Length 1446;					
Best Local Similarity 25.1%; Pred. No. 0.068;					
Matches 93; Conservative 35; Mismatches 129; Indels 113; Gaps 18;					
QY	3 SRRSVKSGPREVPDEYEDLYTTP-----SSGMASPSDPDTSRGA 44				
Db	41 SRRSSG-----BDLFGPGGLRSDDAAEAEAVLAACATATPRRP-----SA 86				
QY	45 LQTSRSGEVRFOYDESD-----YALYGSSSDDEHPEV--PRTT- 85				
Db	87 QQQQQPRRSGEIVLDEDEDEDEPGSPAAGSPERALHQS-----EHGHLVLPGRSPA 141				
QY	86 ----RPVSGAVLVSP-----GPARAP-----PRASGAGAGTPTTAPARTQVATKA 131				
Db	142 GSGPRPPPALAAAEAGACGPGSPGSSPASPASSSSPG--PSAAPRMSPARGDVPG 199				
QY	132 PAAPAAETTRGKSAQEPESALPDPASTAPTRSKTPAQGLARKLHFTAPNPDPAPWTP 191				
Db	200 EPGPARAPRTPARPQ--AAVAAAPARGRSPASPAAGV-----SAPOGGAP--- 248				
QY	192 RVAGNKKRYFCANGRLLAAMH-----RMAAVQLMD-----MSRPTDEDLNEL 236				
Db	249 -SAGGDR-----GRNHNOHREPLLEDPAAARLRIDPRLGARSPVSNPNNSNTTV 300				
QY	237 GITTTRVTVCEGKNLLQANELVNPDVQV-----VDATATATGR---SAASPTERRAP 289				
Db	301 AVEYVAKPEKDEODGLAGDGAGPPQQRPRRRRAGCALRRGRGKSSSSSGSDUSLP 360				

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QY      290 ARSASRP RP 299          ||| ||| |
Db      361 ARSPSA PRAP 370
RESULT_9
ICP3_HSV1F
ID     ICP3_HSV1F    STANDARD:   PRT:   263 AA.
AC     P08353;
DT     01-AUG-1988 (Rel. 08, Created)
DR     01-OCT-1994 (Rel. 30, Last sequence update)
DE     01-OCT-1994 (Rel. 30, Last annotation update)
DE     Infected cell protein ICP34.5 (Neurovirulence factor ICP34.5).
GN     ICP34.5.
OS     Herpes simplex virus (type 1 / strain F).
OC     Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OX     Alphaherpesvirinae; Simplexvirus.
RN     NCBI_TaxID=10304;
[1]
RE     SEQUENCE FROM N.A.
RP     MEDLINE=86115412; PubMed=3003394;
RA     Chou J., Roizman B.;
RT     "The terminal a sequence of the herpes simplex virus genome contains
RT     the promoter of a gene located in the repeat sequences of the L
RT     component.";
RL     J. Virol. 57:629-637(1986).
[2]
RE     REVISIONS.
RX     MEDLINE=90156494; PubMed=2154589;
RA     Chou J., Roizman B.;
RT     "The herpes simplex virus 1 gene for ICP34.5, which maps in inverted
RT     repeats, is conserved in several limited-passage isolates but not in
RT     strain 17synr+.";
RL     J. Virol. 64:1014-1020(1990).
-1- FUNCTION: NOT KNOWN. HAS A PROFOUND EFFECT ON THE GROWTH OF THE
CC     VIRUS IN CENTRAL NERVOUS SYSTEM TISSUE.
CC     -1- SUBCELLULAR LOCATION: CYTOPLASMIC; IN INFECTED CELL.
CC     -1- DEVELOPMENTAL STAGE: ACCUMULATES LATE IN INFECTION.
-----
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-----
DR     EMBL; M12240; AAA45794.1; ALT_SEQ.
DR     EMBL; M33699; AAA45790.1; -.
DR     DDBJ; A27768; WMBB38.
KW     Repeat; Late protein.
FT     DOMAIN              161      190      10 X 3 AA TANDEM REPEATS OF A-T-P.
SQ     SEQUENCE           263 AA; 27533 MW; F5084106A08A8CBI CRC64;
Query Match       9.1%; Score 142.5; DB 1; Length 263;
Best Local Similarity 25.6%; Pred. No. 0.056;
Matches 75; Conservative 24; Mismatches 125; Indels 69; Gaps 15;
QY      2 TSRSVSKGPREVPEDEEDLYTFSSGMAFPSDPDTSRRCALQTRSORGEVFHFVYOD 61
Db      24 TAQSQVTSTPNSEPA-----VKSADPAAPPPPASGPPSCSLLRQ-----MLHP 70
QY      62 ES DYALTYGSSSEDDEHEVPRT-----RPSGVAVLSGPGARAPPPPAGSGGAGRPT 116
Db      71 ES-----ASDDDDDDWDSDSPPEPAPARPAA-----PR-RSPPPAGGG--GANPS 119
QY      117 TAPRAP-----RTGRVTTKAPAAPAAEAETTRKRKSAOPEASALLPPAPASTA-PTRSKTPA 169
Db      120 HPPSRPFPLPRLALRLVTVTAHLAKRLKRRAGGCGAAPPTPATPTATPATPATPAIPA 179
QY      170 QGLARKLFHTAPNPDAFWTPRVAGFNKRVFGCAAVGRLA--AMHARMAAYVLDMMSRRP 227

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-1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF

TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.

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DR EMBL: AF156673; AAF68176.1; -
DR EMBL: AF156603; AAF68174.1; -
DR EMBL: AF245470; AAK20935.1; -
DR EMBL: AF245471; AAK20936.1; -
DR EMBL: AF245472; AAK20937.1; -
DR EMBL: AF245473; AAK20938.1; -
DR EMBL: AF245474; AAK20939.1; -
DR EMBL: AF056184; AAD28084.1; -
DR EMBL: BC012923; AAH12923.1; -
DR MIM: 605678; -
DR MIM: 194050; -
DR HSSP: P25912; IHL0.
DR InterPro: IPR001092; HLH_dlm.
DR InterPro: IPR003015; HLH_Myc.
DR Pfam: PF00010; HLH_1.
DR SMART: SM00353; HLH_1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; 1.
DR Transcription regulation; Repressor; Nuclear protein; DNA-binding;
KM Alternative splicing.
FT DOMAIN 387 394 POLY-PRO.
FT DNA_BIND 409 417 BASIC DOMAIN.
FT DOMAIN 648 662 HELIX-LOOP-HELIX MOTIF (POTENTIAL).
FT DOMAIN 688 702 HELIX-LOOP-HELIX MOTIF (POTENTIAL).
FT DOMAIN 703 724 LEUCINE-ZIPPER.
FT VARSPPLIC 176 268 MISSING (IN ISOFORM 6).
FT VARSPPLIC 558 575 OETVPEPCPEPPTAP -> AVNGCCGCTSAQCAGL
(IN ISOFORM 5).
FT VARSPPLIC 576 852 MISSING (IN ISOFORM 5).
FT VARSPPLIC 647 648 MISSING (IN ISOFORM 3 AND ISOFORM 4).
FT VARSPPLIC 687 705 MISSING (IN ISOFORM 2 AND ISOFORM 4).
FT VARSPPLIC 814 815 TV -> ST (IN ISOFORM 6).
FT VARSPPLIC 816 852 MISSING (IN ISOFORM 6).
FT CONFLICT 558 558 MISSING (IN REF. 4).
SQ SEQUENCE 852 AA; 93071 MW; D49E3C3D7C0A72EC CRC64;

Query Match 8.6%; Score 133.5; DB 1; Length 852;
Best Local Similarity 22.7%; Pred. No. 0.56; Mismatches 117; Indels 145; Gaps 14;
Matches 85; Conservative 27;

QY 27 SSGMASPDSPDTSR-----RGALQTRSRQGEVRFVQYDESDYALYGSSSEDEHP 80
Db 332 SSGTLEGPVPPASSAMTHLSGHSRLQARNSCOPGLDSSAFLLSDFLL-----PE 380
QY 81 VPRRR---RVSGAVLSGPPRAPR-----PPRAGSGA----- 111
Db 381 DPKRLPPPPVPPPLHYPPRAKVPGLPCPPPPPPMAPPTALLDEPLESPRPPTV 440
QY 112 -----GRTPTTAPRA--PRTORVATKAP-----AAPAETT 140
Db 441 PPAAGVPLPAFAFPPTPSPVSPATPPPIELLPLGYSEPAFGCFSPMRGKPPAPSP 500
QY 141 RGRKSAOPESALPDAFASTAPTR-----SKTPAOGIARKLHST----- 180
Db 501 RQGKASPTLPATVATSPPTANNPCLTQULTLAKPEQALEPPLVSTLLRSPGPOET 560
QY 181 -----APPNDAPMTPRVAGNKRVCANVGRLLAAMARMAAVOLMDMSRP----- 226
Db 561 VPEPCTFLPPTP-APRPPR-----PPGPATLAPSRPLVKAERLSPAPSGS 609
QY 227 --RTDELNELGTTTIRVTVCEGKNLORANELVNDPVQDVDAATATGSAASRPT 284
Db 610 ERRLSGDLSSMPGCGTILSVKVSPPPIILSRG-----RPD-----SKMTE 648

QY 285 RPRAPARSAPRR 298
Db 649 NRRITHISAQKRR 662

RESULT 14
GSRL_HUMAN
ID GSRL_HUMAN STANDARD; PRT; 1509 AA.
AC G9NZM4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glioma tumor suppressor candidate region gene 1 protein.
GN GLTSCR1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=20175430; PubMed=10708517;
RA Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
RA Portler B.P., Ueki K., Billings S., Ramasamy S., Mohrenweiser H.W.,
RA Scheithauer B.W., Louis D.N., Jenkins R.B.;
RT "A transcript map of the chromosome 19q-Arm glioma tumor suppressor
RT region.";
RL Genomics 64:44-50(2000).
CC -!- TISSUE SPECIFICITY: Expressed at moderate levels in heart, brain,
CC placenta, skeletal muscle, and pancreas, and at lower levels in
CC lung, liver, and kidney.
CC -----
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DR EMBL: AF182077; AAF62874.1; -
DR MIM: 605690; -
FT DOMAIN 37 45 POLY-GLY.
FT DOMAIN 884 889 POLY-PRO.
FT DOMAIN 1214 1225 POLY-SER.
FT DOMAIN 1282 1286 POLY-PRO.
FT DOMAIN 1294 1304 POLY-PRO.
SQ SEQUENCE 1509 AA; 152991 MW; 7C5144F443CE6821 CRC64;

Query Match 8.5%; Score 133; DB 1; Length 1509;
Best Local Similarity 28.5%; Pred. No. 1;
Matches 53; Conservative 21; Mismatches 70; Indels 42; Gaps 10;

QY 26 PSSGMA-SPD-----SPDTSRKALQTRSRQGEVRFVQYDESDYALYGSSSEDEHP 79
Db 615 PSEGLASSPEKIVLGGPPSATPTAILQDSIQ-----MFLQERSQDPL-----SAEGRHL 665
QY 80 EVPTRRVSGAVLSGPPRAPRP--PAGSG-CAGRTPTTAPRAPRTORVATKAPAPA 136
Db 666 SVP-----ASVYSAPRPQODRAPATPVAKGAGLG-----PQAPDSQASPARAPDIPA 713
QY 137 AETTRG-----RKSAPESALPDAFASTAPTRSKTPAOGIARKLHSTAP-----PN 184
Db 714 AAPLKGPPSSPPLPHQAPLGDSPHLRPHPTRPSPRSRPSQSVSRPSEPLHPCRP 773
QY 185 PDAPMT 190
Db 774 PQAPPT 779

RESULT 15
PAK4_HUMAN

ID PAK4_HUMAN STANDARD; PRT; 591 AA.
 AC 096013; 09B033;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase PAK 4 (EC 2.7.1.-) (p21-activated kinase 4) (PAK-4).
 GN PAK4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBITaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=99043860; PubMed=9822598;
 RA Abo A., Ou J., Cammarano M.S., Dan C., Fritsch A., Baud V., Bellisle B., Mladen A.;
 RT "PAK4, a novel effector for Cdc42hs, is implicated in the reorganization of the actin cytoskeleton and in the formation of filopodia."
 RT EMBO J. 17:6527-6540(1998).
 RL [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RA Melnick M.B.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases. [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Eye, and Placenta;
 RA Strusberg R.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTIVATES THE JNK PATHWAY. IMPLICATED IN THE REORGANIZATION OF THE ACTIN CYTOSKELETON AND IN THE FORMATION OF FILOPODIA.
 CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND WEAKLY WITH RAC1.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; may be produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN PROSTATE, TESTIS, AND COLON.
 CC -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. STE20 SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 GBD DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: A011855; CA09820.1; -
 DR EMBL: AF05046; AAD01210.1; -
 DR EMBL: BC002921; AAH02921.1; -
 DR EMBL: BC011368; AAH11368.1; -
 DR HSSP: P00518; 1PHK.
 DR MIM: 605451; -
 DR InterPro: IPR000719; Euk_kinase.
 DR InterPro: IPR000095; PAK_box_P21_Rho_binding.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00786; PBD; 1.
 DR Pfam: PF00069; PKinase; 1.
 DR SMART: SM00285; PBD; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS0108; GBD; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE NEG.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Alternative splicing.
 FT DOMAIN 11 46 GBD.
 FT 47 320 LINKER.

FT DOMAIN 321 572 PROTEIN KINASE.
 FT NP_BIND 327 335 ATP (BY SIMILARITY).
 FT BINDING 350 350 ATP (BY SIMILARITY).
 FT ACT_SITE 440 440 BY SIMILARITY.
 FT VARSPIC 120 120 E -> K (IN ISOFORM 2).
 FT VARSPIC 121 285 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 591 AA; 64071 MW; 04C2A5C0B06427D5 CRC64;

Query Match 8 4%; Score 130.5; DB 1; Length 591;
 Best Local Similarity 23.0%; Pred. No. 0.58; Indels 107; Gaps 17;
 Matches 82; Conservative 43; Mismatches 125;

QY 5 RSVSGPREVPREDVEDLYTPSSGM-----ASPDSPDTSRGLQTRS 49
 Db 75 KGAKDGLTLTLDDEFEMSVTRSNLSLRDSPPPARARQENGMEEPATTARGPGRAGS 134
 QY 50 RQGEVRFVQYDESDVALYGGSSSEDEHPEV-PRTRPVSGAVLSGP-----G 97
 Db 135 RG----RFAGHSEAG---GGSGDRRRAGCEKRPKSSREGSG---GPOESSRDKRPLSG 182
 QY 98 PARAPPPAG--SG---GAGRTPTTAPRA----- 121
 Db 183 PDVGTQPGAGIASGAKLAAGRPPENTYPRADTDHPSRGAQGEPHDVADNGSAGGLAIPQS 242
 QY 122 -PTQVATKAPAPAPAAETTRGRKSAQE---SAALPDAPASTAPTRSKTPAOGIARKLH 177
 Db 243 SSSSRPPTARAGAPSPGV-L-GHASEPOLAPACTTAALAAVAPGPPRPQRPQGVSH 301
 QY 178 -ESTAPNPDAEPWTPR-----VAGFNKRVFCAAVGRLAAMHARMAAVQIWMDSRPR 227
 Db 302 EQFRALQLVDDPDPRSILDNFIKIGEGSTGICTIVRSS---GLTAVKKMDLRK-- 356
 QY 228 TDEILNLLGTTIRVYCGEKNLQKANELVMPD---VQD-----VDAATATR 274
 Db 357 --QQRRELFENEVYIMRDYQENVEVMSYLVGDDELVMFELEGALDIYVTHR 411

Search completed: August 28, 2002, 12:27:59
 Job time: 238 sec

XX Fusion and chimaeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
XX
PS Example 2: Page 27: 88pp: English.
XX
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a
CC CDK, linked to a transcription regulator functional in eukaryotic cells;
CC (ii) second gene construct comprising a sequence encoding a polypeptide
CC that promotes endotheialisation, and (iii) a gene delivery composition
CC for delivering the GCS to a cell for transfection. Also provided are
CC nucleic acids encoding a fusion protein (FP) containing: (i) a
CC therapeutic polypeptide sequence (TP) from an intracellular protein that
CC alters a cellular process when FP enters the cell, and (ii) a
CC transcellular polypeptide sequence (TCP) that promotes transcytosis of
CC FP. The FP consists of at least one CDK-binding motif and a TCP. See
CC AAX26220 for detailed uses of the recombinant transfection system. The
CC CKI polypeptides are engineered to include any of the peptides shown in
CC AAW5097-100 encoded by the DNA sequences AAX26225-228.
XX
SQ Sequence 37 AA:

Query Match 11.5%: Score 179; DB 20: Length 37;
Best Local Similarity 100.0%: Pred. No. 4.4e-08;
Matches 36: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 266 DVDATATGRGSAASRPTERRPARASASRRPRVE 301
DB 2 dvdaatatgrgsaasrpterrparasaarprpve 37
|||||

RESULT 2
AA96575
ID AAY96575 standard; Protein: 37 AA.
XX
AC AAY96575:
XX
XX 12-SEP-2000 (first entry)
XX
DE HSV-1 VP22 polypeptide C-terminal domain.
XX
XX
KW hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW proliferation; immortal; tumour therapy; macular degeneration; activator;
KW INK4; HSV-1; VP22; fusion protein.
XX
XX
OS Herpes simplex virus 1.
XX
PN WO200031238-A2.
XX
PD 02-JUN-2000.
XX
XX
PF 24-NOV-1999; 99WO-US27907.
XX
PR 25-NOV-1998; 98US-0109891.
PR 17-FEB-1999; 99US-0120549.
XX
XX
PA (GENE-) GENETICA INC.
XX
PI Hannon GJ, Beach DH;
XX
XX WPI: 2000-400055/34.
DR N-PSDB: AAA29396.
XX
XX
PT New method for increasing the proliferative capacity of cell lines
PT comprising administering agents reversibly activating telomerase

PT activity and reversibly inactivating Rb/INK4 and/or p53 pathways useful
PT in treating age related diseases
XX
XX Disclosure; Page 32; 123pp: English.
XX
CC The HSV-1 VP22 polypeptide can be fused to a retinoblastoma (Rb)
CC inactivator protein sequence to aid targeting and internalization.
CC The invention concerns methods and reagents for extending the life-span,
CC e.g. the number of mitotic divisions, of a cell. The method relies on
CC activation of a telomerase activity and inhibition of one or both of a
CC Rb/INK4 pathway or a p53 pathway. Phosphorylation of Rb by
CC cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
CC division cycle. Binding of INK4 family members, e.g. the tumour
CC suppressor p16INK4a, inhibits kinase activity and results in growth
CC arrest. Rb inactivators can selectively and reversibly inactivate an
CC Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
CC is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
CC and can also be used in the methods. Other molecules which can be used
CC include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
CC differs from at one or more of residues K22, R24, H95 and/or D97.
CC Additional constructs include a papilloma virus E7 protein, or other
CC viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
CC the Rb and p16INK4a genes may also be used. The methods are useful for
CC increasing the proliferative capacity of cells. The cells are
CC subsequently of use in pharmaceutical and cosmetic preparations used to
CC treat conditions related to (premature) ageing, e.g. macular degeneration
CC and arteriosclerosis. The cells can also be used to replace tumour cell
CC lines in vitro and for studies on biochemical and physiological aspects
CC of growth and differentiation. Long lived (immortal) cells could also be
CC of use in the production of normal or genetically engineered
CC biotechnology products.
XX
SQ Sequence 37 AA:

Query Match 11.5%: Score 179; DB 21: Length 37;
Best Local Similarity 100.0%: Pred. No. 4.4e-08;
Matches 36: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 266 DVDATATGRGSAASRPTERRPARASASRRPRVE 301
DB 2 dvdaatatgrgsaasrpterrparasaarprpve 37
|||||

RESULT 3
AA83262
ID AAY83262 standard; Protein: 37 AA.
XX
XX
AC AAY83262:
XX
XX 16-AUG-2000 (first entry)
XX
DE HSV-1 V22 C-terminal peptide.
XX
XX
KW ubiquitin ligase; SCF; F-box protein; targeted degradation;
KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;
KW oncoprotein; Huntington's disease; gene knockout; delivery systems.
XX
XX
OS Synthetic.
XX
PN WO200022110-A2.
XX
PD 20-APR-2000.
XX
XX
PF 08-OCT-1999; 99WO-US23705.
XX
PR 09-OCT-1998; 98US-0103787.
XX
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Zhou P, Howley P;
XX
XX

PT	Use of papillomavirus E2 protein peptidomimetics for treating
PT	papillomavirus-infected cells and papillomavirus-induced conditions in
PT	mammals by inhibiting E1-E2 interaction
XX	
PS	Disclosure: Page 43; 110pp; English.
XX	
CC	The present invention describes the use of a small organic compound (A)
CC	which competitively inhibits interaction of a papillomavirus (PV) E2
CC	protein with a PV E1 protein for treating a cell infected with PV or a
CC	mammal with a PV-induced condition. (A) has antiviral, virucide,
CC	cytostatic, antiproliferative and dermatological activities. Methods
CC	from the present invention can be used to treat PV-induced conditions
CC	including growth of PV preneoplastic and neoplastic lesions, cutaneous
CC	lesions chosen from warts and other benign cutaneous lesions, plantar
CC	warts (verruca plantaris), common warts (verruca plana), Butcher's
CC	common warts, flat warts, genital warts (condyloma acuminatum) and
CC	epidermodysplasia verruciformis, laryngeal, oral, pharyngeal,
CC	oesophagel and other upper airway papilloma or vaginal, cervical,
CC	vulvar, penile and anoectal carcinoma. The E2 inhibitors may also be
CC	used to treat epithelial and internal fibropapillomas in animals.
CC	The present sequence represents a peptide sequence used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 37 AA:
QY	Query Match 11.5%; Score 179; DB 21; Length 37;
	Best Local Similarity 100.0%; Pred. No. 4,4e-06;
	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	266 DVDAATATGCRSAASRPTEPRAPARSASRP RPVE 301
	2 dvdaatatrgtsaasrptcrpraparsasrptprve 37
RESULT 5	
XX	AAB60911
ID	AAB60911 standard; Peptide: 37 AA.
XX	AAB60911;
XX	
DT	05-NOV-2001 (first entry)
XX	
DE	HSV-1 VP22 C-terminus.
XX	
KW	Co-activator domain; P300/CBP KIX domain; erythrocythaemia; skin disease;
KW	polycythaemia; haemoglobinopathy; cell differentiation; ulcer; cancer;
KW	neurological condition; neurodegenerative disease; immune disease;
KW	diabetes.
XX	
OS	Synthetic.
XX	
PN	WO200118036-A2.
PD	
XX	15-MAR-2001.
XX	
FE	31-AUG-2000; 2000WO-US24010.
XX	
PR	03-SEP-1999; 99US-0152402.
XX	
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PA	(JOSL-) JOSLIN DIABETES CENT INC.
PI	
PI	Frangioni JV, Cantley LC, Montminy MR;
XX	
DR	WPI: 2001-273380/28.
DR	N-PSDB: AAF58997.
XX	
PT	Identifying co-activator domain specific transcriptional activators by
PT	contacting a target domain of a selected transcription factor with a
PT	peptide display library, where the identified binding peptides are
PT	useful for reducing hyperglycemia
XX	

PS Disclosure; page 79; 156pp; English.

XX The present invention describes a method of identifying the co-activator
 CC domain of specific synthetic activators, involving contacting the target
 CC domain of a selected transcription factor with a peptide display library,
 CC and identifying those sequences which bind to the target domain. In
 CC particular, those which bind to the KIX domain of p300/CBP are useful.
 CC The peptides can be used in the treatment of diseases related to aberrant
 CC KIX-dependent gene transcription, including erythrocythaemia,
 CC polycythaemia, haemoglobinopathies, to regulate cell differentiation, to
 CC treat neurological diseases, immunological diseases, diabetes, ulcers,
 CC skin diseases and cancer, and to aid wound healing. The present sequence
 CC is a peptide described in the exemplification of the invention.

XX Sequence 37 AA:

XX

Query Match 11.5%; Score 179; DB 22; Length 37;
 Best Local Similarity 100.0%; Pred. No. 4.4e-08;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 266 DVDAATATRCGSAASRPTERRAPARSASRRPRPVE 301
 |||||||
 DB 2 dvdaaatatrgsaastrpterraparsasrrprpve 37

RESULT 6
 AAE12206
 ID AAE12206 standard; peptide; 34 AA.

XX AAE12206:

XX 18-DEC-2001 (first entry)

XX Membrane transport sequence of herpes simplex virus type 1.

DE

XX Polyglutamine repeat domain; huntingtin; atrophin; ataxin;
 KW androgen receptor protein; neurodegenerative disease; anticonvulsant;
 KW Huntington's disease; dentatorubral pallidoluysian atrophy; DRPLA;
 KW spinobulbar muscular atrophy; spinocerebellar ataxia; noctropic;
 KW membrane transport sequence.

XX Herpes simplex virus type 1.

OS

XX WO200168678-A2.

PN

XX 20-SEP-2001.

PD

XX 14-MAR-2001: 2001WO-US08222.

PF

XX 16-MAR-2000: 2000US-189781P.

PR

XX (UYDU-) UNITV DUKE.

PA

XX Strittmatter WJ, Burke JR, Nagai Y;

PI

XX WPI: 2001-616285/71.

DR

XX New polyglutamines which selectively bind to expanded polyglutamine
 PT repeat domains, useful for treating neurodegenerative diseases, e.g.
 PT Huntington's disease -

PT

XX

XX

PS Example 14; Page 59; 59pp; English.

XX The present sequence is a membrane transport sequence of
 CC herpes simplex virus type 1 which is fused to the polyglutamine binding
 CC peptide. The peptide is useful for treating a cell that contains and
 CC expresses a protein having an expanded polyglutamine region (e.g.
 CC huntingtin; atrophin 1, ataxin 1, 2, 6 or 7; or androgen receptor
 CC protein), or treating a neurodegenerative disease characterised by the
 CC presence of expanded polyglutamine repeats, e.g. Huntington's disease,
 CC dentatorubral pallidoluysian atrophy (DRPLA), spinobulbar muscular
 CC atrophy, and spinocerebellar ataxia types 1, 2, 3, 6 and 7.

XX Sequence 34 AA:

SQ

Query Match 10.6%; Score 166; DB 22; Length 34;
 Best Local Similarity 97.1%; Pred. No. 4.7e-07;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 268 DAATATRCGSAASRPTERRAPARSASRRPRPVE 301
 |||||||
 DB 1 daatatrgsaastrpterraparsasrrprpvd 34

RESULT 7
 AAM47198
 ID AAM47198 standard; peptide; 20 AA.

XX AAM47198:

XX 03-JUL-1998 (first entry)

XX HSV truncated tegument protein VP22 derived peptide C.

DE

XX HSV, tegument protein; VP22; UL49; antiviral agent; treatment;
 KW cold sore; genital herpes; chickenpox; shingles.

KW

XX Herpes simplex virus.

OS

XX Synthetic.

XX WO9804708-A1.

PN

XX 05-FEB-1998.

PD

XX 28-JUL-1997: 97WO-GB02036.

PF

XX 26-JUL-1996: 96GB-0015726.

PR

XX (MED-) MEDICAL RES COUNCIL.

PA

XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HMM;

PI

XX WPI: 1998-130696/12.

DR

XX New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox

PT

XX

XX Example; Page 25; 75pp; English.

PS

XX The present sequence is a herpes simplex virus (HSV) truncated
 CC tegument protein VP22 derived peptide. VP22 was used in the
 CC preparation of a novel antiviral agent, which inhibits the
 CC maturation and/or replication of HSV by disrupting association
 CC between VP22 and VP16 and/or gB. The agent can be used to treat,
 CC e.g. cold sores, genital herpes, chickenpox and shingles.

CC

XX

SQ Sequence 20 AA:

Query Match 7.5%; Score 117; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 178 FSTAPPNDAPWTPRVAGFN 197
 |||||||
 DB 1 fstappndapwtprvagfn 20

RESULT 8
 AAM47197
 ID AAM47197 standard; peptide; 20 AA.

XX AAM47197:

XX 03-JUL-1998 (first entry)
DE HSV truncated tegument protein VP22 derived peptide B.
XX
XX HSV, tegument protein; VP22; UL49; antiviral agent; treatment;
KM cold sore; genital herpes; chickenpox; shingles.
XX
OS Herpes simplex virus.
XX Synthetic.
XX
XX WO9804708-A1.
XX
XX 05-FEB-1998.
XX
XX 28-JUL-1997; 97WO-GB02036.
XX
XX 26-JUL-1996; 96GB-0015726.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HM.
XX
XX WPI; 1998-130696/12.
XX
XX New antiviral agent disrupting binding of VP22 to VP16 or gB -
PI useful for treating infections caused by herpes simplex, e.g. cold
PT sores and chicken-pox
XX
XX Example; Page 25; 75pp; English.
XX
XX The present sequence is a herpes simplex virus (HSV) truncated
CC tegument protein VP22 derived peptide. VP22 was used in the
CC preparation of a novel antiviral agent, which inhibits the
CC maturation and/or replication of HSV by disrupting association
CC between VP22 and VP16 and/or gB. The agent can be used to treat,
CC e.g. cold sores, genital herpes, chickenpox and shingles.
XX
XX Sequence 20 AA:
SQ

Query Match 6.9%; Score 108; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 KTPAGGLARKLHSTAPPNP 185
Db 1 ktpagglarklhfstappnp 20

RESULT 9
AAW47201
ID AAW47201 standard; peptide; 20 AA.
XX
XX AAW47201;
AC
XX
XX 03-JUL-1998 (first entry)
DE HSV truncated tegument protein VP22 derived peptide F.
XX
XX HSV, tegument protein; VP22; UL49; antiviral agent; treatment;
KM cold sore; genital herpes; chickenpox; shingles.
XX
OS Herpes simplex virus.
XX Synthetic.
XX
XX WO9804708-A1.
XX
XX 05-FEB-1998.
XX
XX 28-JUL-1997; 97WO-GB02036.
XX
XX 26-JUL-1996; 96GB-0015726.
XX
XX

XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HM;
XX
XX WPI; 1998-130696/12.
XX
XX New antiviral agent disrupting binding of VP22 to VP16 or gB -
PI useful for treating infections caused by herpes simplex, e.g. cold
PT sores and chicken-pox
XX
XX Example; Page 25; 75pp; English.
XX
XX The present sequence is a herpes simplex virus (HSV) truncated
CC tegument protein VP22 derived peptide. VP22 was used in the
CC preparation of a novel antiviral agent, which inhibits the
CC maturation and/or replication of HSV by disrupting association
CC between VP22 and VP16 and/or gB. The agent can be used to treat,
CC e.g. cold sores, genital herpes, chickenpox and shingles.
XX
XX Sequence 20 AA:
SQ

Query Match 6.8%; Score 106; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 RMAAVQLMDMSRPRTDEDIN 233
Db 1 rmaavqlmdmsrprdedin 20

RESULT 10
AAW47200
ID AAW47200 standard; peptide; 20 AA.
XX
XX AAW47200;
AC
XX
XX 03-JUL-1998 (first entry)
DE HSV truncated tegument protein VP22 derived peptide E.
XX
XX HSV, tegument protein; VP22; UL49; antiviral agent; treatment;
KM cold sore; genital herpes; chickenpox; shingles.
XX
OS Herpes simplex virus.
XX Synthetic.
XX
XX WO9804708-A1.
XX
XX 05-FEB-1998.
XX
XX 28-JUL-1997; 97WO-GB02036.
XX
XX 26-JUL-1996; 96GB-0015726.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HM;
XX
XX WPI; 1998-130696/12.
XX
XX New antiviral agent disrupting binding of VP22 to VP16 or gB -
PI useful for treating infections caused by herpes simplex, e.g. cold
PT sores and chicken-pox
XX
XX Claim 10; Page 25; 75pp; English.
XX
XX The present sequence is a herpes simplex virus (HSV) truncated
CC tegument protein VP22 derived peptide. VP22 was used in the
CC preparation of a novel antiviral agent, which inhibits the
CC maturation and/or replication of HSV by disrupting association
CC between VP22 and VP16 and/or gB. The agent can be used to treat,
XX

CC e.g. cold sores, genital herpes, chickenpox and shingles.
 XX
 SQ Sequence 20 AA;

Query Match 6.6%; Score 103; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 202 CAVGRILAAHARMAAVOLM 221
 ||||||||||||||||
 Db 1 caavgrilaaharmaavqlw 20

RESULT 11
 AAM47199
 ID AAM47199 standard; peptide; 20 AA.

XX AAM47199;
 AC
 XX
 DT 03-JUL-1998 (first entry)
 XX
 DE HSV truncated tegument protein VP22 derived peptide D.
 XX
 KW HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
 KW cold sore; genital herpes; chickenpox; shingles.
 OS Herpes simplex virus.
 OS Synthetic.
 XX
 PN WO9804708-A1.
 PD
 XX 05-FEB-1998.
 PF 28-JUL-1997; 97WO-GB02036.
 PR 26-JUL-1996; 96GB-0015726.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Hope RG, McGeoch DJ, McLaughlan J, Rixon HMM;
 XX
 DR WPI; 1998-130696/12.
 XX
 PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox
 XX
 PS Claim 5; Page 25; 75pp; English.
 XX
 CC The present sequence is a herpes simplex virus (HSV) truncated
 CC tegument protein VP22 derived peptide. VP22 was used in the
 CC preparation of a novel antiviral agent, which inhibits the
 CC maturation and/or replication of HSV by disrupting association
 CC between VP22 and VP16 and/or gB. The agent can be used to treat,
 CC e.g. cold sores, genital herpes, chickenpox and shingles.
 XX
 SQ Sequence 20 AA;

Query Match 6.6%; Score 103; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 190 TPRVAGFNKRVCFAVGRILA 209
 ||||||||||||||||
 Db 1 tprvagfnkrvcfaavgrila 20

RESULT 12
 AAM47203
 ID AAM47203 standard; peptide; 20 AA.
 XX

AC AAM47203;
 XX
 DT 03-JUL-1998 (first entry)
 XX
 DE HSV truncated tegument protein VP22 derived peptide H.
 XX
 KW HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
 KW cold sore; genital herpes; chickenpox; shingles.
 OS Herpes simplex virus.
 OS Synthetic.
 XX
 PN WO9804708-A1.
 PD
 XX 05-FEB-1998.
 PF 28-JUL-1997; 97WO-GB02036.
 PR 26-JUL-1996; 96GB-0015726.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Hope RG, McGeoch DJ, McLaughlan J, Rixon HMM;
 XX
 DR WPI; 1998-130696/12.
 XX
 PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox
 XX
 PS Claim 5; Page 25; 75pp; English.
 XX
 CC The present sequence is a herpes simplex virus (HSV) truncated
 CC tegument protein VP22 derived peptide. VP22 was used in the
 CC preparation of a novel antiviral agent, which inhibits the
 CC maturation and/or replication of HSV by disrupting association
 CC between VP22 and VP16 and/or gB. The agent can be used to treat,
 CC e.g. cold sores, genital herpes, chickenpox and shingles.
 XX
 SQ Sequence 20 AA;

Query Match 6.4%; Score 100; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.077;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 238 ITTIRVTGEGKNLQRPANE 257
 ||||||||||||||||
 Db 1 ittirvtcegnknlqrpane 20

RESULT 13
 AAM47202
 ID AAM47202 standard; peptide; 20 AA.

XX AAM47202;
 AC
 XX
 DT 03-JUL-1998 (first entry)
 XX
 DE HSV truncated tegument protein VP22 derived peptide G.
 XX
 KW HSV; tegument protein; VP22; UL49; antiviral agent; treatment;
 KW cold sore; genital herpes; chickenpox; shingles.
 OS Herpes simplex virus.
 OS Synthetic.
 XX
 PN WO9804708-A1.
 PD
 XX 05-FEB-1998.
 PF 28-JUL-1997; 97WO-GB02036.
 XX

PR 26-JUL-1996: 96GB-0015726.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Hope RG, McGeoch DJ, McLaughlan J, Rixon HMW;
 XX
 DR WPI: 1998-130696/12.
 XX
 PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox
 PS
 XX Example; Page 25; 75pp; English.
 XX
 CC The present sequence is a herpes simplex virus (HSV) truncated
 CC tegument protein VP22 derived peptide. VP22 was used in the
 CC preparation of a novel antiviral agent, which inhibits the
 CC maturation and/or replication of HSV by disrupting association
 CC between VP22 and VP16 and/or gB. The agent can be used to treat,
 CC e.g. cold sores, genital herpes, chickenpox and shingles.
 XX
 SO Sequence 20 AA:

Query Match 6.3%; Score 99; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.093;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 PRDDELDNELGITTIRVTV 245
 |||||
 DB 1 prdedlnelgittirv tv 20

RESULT 14

AAW47204
 ID AAW47204 standard; peptide; 20 AA.

AC AAW47204;

DT 03-JUL-1998 (first entry)

DE HSV truncated tegument protein VP22 derived peptide I.

XX HSV; tegument protein; VP22; UL49: antiviral agent; treatment;

KW cold sore; genital herpes; chickenpox; shingles.

XX Herpes simplex virus.

OS Synthetic.

XX MO9804708-A1.

PD 05-FEB-1998.

PF 28-JUL-1997: 97WO-GB02036.

PR 26-JUL-1996: 96GB-0015726.

PA (MEDI-) MEDICAL RES COUNCIL.

XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HMW;

DR WPI: 1998-130696/12.

PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox
 PS
 XX Example; Page 25; 75pp; English.

CC The present sequence is a herpes simplex virus (HSV) truncated
 CC tegument protein VP22 derived peptide. VP22 was used in the
 CC preparation of a novel antiviral agent, which inhibits the
 CC maturation and/or replication of HSV by disrupting association

CC between VP22 and VP16 and/or gB. The agent can be used to treat,
 CC e.g. cold sores, genital herpes, chickenpox and shingles.
 XX
 SO Sequence 20 AA:

Query Match 5.7%; Score 89; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 NLLQANELVNDVVQDV 267
 |||||
 DB 1 nllgranelvndvvqv dv 18

RESULT 15

AAW47196
 ID AAW47196 standard; peptide; 20 AA.

AC AAW47196;

DT 03-JUL-1998 (first entry)

DE HSV truncated tegument protein VP22 derived peptide A.

XX HSV; tegument protein; VP22; UL49: antiviral agent; treatment;

KW cold sore; genital herpes; chickenpox; shingles.

XX Herpes simplex virus.

OS Synthetic.

XX MO9804708-A1.

PD 05-FEB-1998.

PF 28-JUL-1997: 97WO-GB02036.

PR 26-JUL-1996: 96GB-0015726.

PA (MEDI-) MEDICAL RES COUNCIL.

XX Hope RG, McGeoch DJ, McLaughlan J, Rixon HMW;

DR WPI: 1998-130696/12.

PT New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox
 PS
 XX Example; Page 25; 75pp; English.

CC The present sequence is a herpes simplex virus (HSV) truncated
 CC tegument protein VP22 derived peptide. VP22 was used in the
 CC preparation of a novel antiviral agent, which inhibits the
 CC maturation and/or replication of HSV by disrupting association
 CC between VP22 and VP16 and/or gB. The agent can be used to treat,
 CC e.g. cold sores, genital herpes, chickenpox and shingles.
 XX

SO Sequence 20 AA:

Query Match 4.7%; Score 73; DB 19; Length 20;
 Best Local Similarity 93.8%; Pred. No. 14;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 158 ASTAPTRSKTPAQGLA 173
 |||||
 DB 5 astaptrsktpaqgla 20

Search completed: August 28, 2002, 12:28:33
 Job time: 247 sec

• • • •

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:18:16 ; Search time 30.53 seconds

(without alignments)
1095.094 Million cell updates/sec

Title: US-09-522-278b-12

Perfect score: 1561

Sequence: 1 MTSRSKSVKSGPREVPDEYE.....PRPRAPANSASRPAPVE 301

Scoring table: BLOSUM62

Searched: 747574 seqs, 111073796 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : A_Geneseq_032802.*

Listing first 45 summaries

1: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
8: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
9: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
10: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1561	100.0	301	AAV42292	Herpes simplex vir
2	1561	100.0	301	AAV27404	HSV-1 tegument pro
3	1561	100.0	301	AAAB6329	VP22 protein fragm
4	1561	100.0	301	AAAG4275	Herpes simplex vir
5	1561	100.0	667	AAE05266	VP22-Cre fusion pr
6	1561	100.0	747	AAE05267	VP22-F1pe fusion p
7	1557	99.7	683	AAE05273	VP22Crestreptag fu
8	1554	99.6	301	AAW95099	HIV-1 VP22 polypep
9	1554	99.6	301	AAV79877	HSV-1 VP22 peptide
10	1554	99.6	301	AAAB60910	HSV-1 VP22 protein
11	1553	99.5	301	AAW47194	Herpes simplex vir

12	1553	99.5	301	21	AAV83261	HSV-1 V22 cellular
13	1520	97.4	297	21	AAV96574	HSV-1 VP22 polypep
14	1392	89.2	267	22	AAAB6330	VP22 protein fragm
15	1203.5	77.1	246	21	AAV78333	Herpes simplex vir
16	1014.5	65.0	306	20	AAAB6755	HSV-2 VP22 protein
17	1006.5	64.5	302	19	AAW72214	HSV-2 strain SB5 C
18	738	47.3	539	22	AAE05270	Delta VP22Cre-Stre
19	573	36.7	144	19	AAW47195	Herpes simplex vir
20	492	31.5	117	19	AAW72068	HSV-2 strain SB5 C
21	323	20.7	131	19	AAW72069	HSV-2 strain SB5 C
22	277	17.7	257	15	AAAB63461	Deduced AA sequenc
23	271.5	17.4	258	21	AAAB0762	Amino acid sequenc
24	205	13.1	249	16	AAAB65493	Marek's disease vi
25	179	11.5	37	20	AAW95100	HIV-1 VP22 polypep
26	179	11.5	37	21	AAV96575	HSV-1 VP22 polypep
27	179	11.5	37	21	AAV93262	HSV-1 V22 C-termin
28	179	11.5	37	21	AAV79878	HSV-1 VP22 C-termin
29	179	11.5	37	22	AAAB60911	HSV-1 VP22 C-termin
30	172.5	11.1	139	18	AAW23003	Canine herpesvirus
31	172.5	11.1	139	19	AAW72663	Canine herpes viru
32	172.5	11.1	139	22	AAAB51320	Canine herpes viru
33	168.5	10.8	451	22	AAAB6528	Human novel cytol
34	166	10.6	34	22	AAE12206	Human novel cytol
35	149.5	9.6	550	22	AAAB82807	Membrane transport
36	149.5	9.6	3119	19	AAW72204	Human low density
37	143.5	9.2	538	22	AAAB82806	HSV-2 strain SB5 C
38	143.5	9.2	889	22	AAAB6461	Human HCN2 protein
39	142.5	9.1	263	13	AAAB21706	HSV-1 (F) ICP34.5
40	141	9.0	258	14	AAAB50049	ICP34.5 fragment
41	135.5	8.7	1243	22	ABG21221	Novel human diagno
42	133.5	8.6	318	22	ABG19764	Novel human diagno
43	132.5	8.5	833	21	AAV55616	Murine nurse cell
44	132.5	8.5	833	22	AAAB60392	Mouse nurse cell
45	132	8.5	863	22	AAAB6463	Murine HCN2 protei

ALIGNMENTS

RESULT 1	
AAV42292	standard; Protein: 301 AA.
ID	AAV42292
AC	AAV42292;
XX	
DT	06-DEC-1999 (first entry)
XX	
DE	Herpes simplex virus type 1 (HSV-1) VP22 tegument protein.
KW	Cytochrome; targeting; localisation; cancer; tumour; produg; reduction;
KW	nucleus.
XX	
OS	Herpes simplex virus type 1.
OS	Synthetic.
XX	
FT	Key
FT	Misc-difference 251..267
FT	location/Qualifiers
PD	10-SEP-1999.
XX	
XX	05-MAR-1999; 99WO-GB00674.
PR	06-MAR-1998; 98GB-0004841.
PR	19-AUG-1998; 98GB-0018103.
PR	29-JAN-1999; 99GB-0002081.
XX	
PA	(OXFO-) OXFORD BIOMEDICA UK LTD.
XX	
PI	Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths LJ,
PI	Mitropoulos K;

Note: "Corresponding DNA sequence appears to be absent"

XX WPI: 1999-551046/46.
DR N-PSDB: AA219784.

XX New produg activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors -

XX Example 7; Fig 3; 187pp: English.

XX This sequence represents a Herpes simplex virus type 1 (HSV-1)
XX VP22 tegument protein, which is involved in transcellular
XX localisation. VP22 can be fused to cytochrome P450 reductase (P450R)
XX derivatives such as anionless P450R (AA142287) or FN fragment
XX (AA142288). This enables the fusion protein to be delivered to
XX neighbouring cells where it is then transported to the nucleus. Many
XX drugs' sites of action are in the nucleus, rather than the cytoplasm,
XX where P450R normally functions. P450R or its derivatives can be used to
XX activate produgs to their active form via reduction. Administration of a
XX produg is useful where the active drug may be metabolised before it
XX reaches its site of action or where the active drug is cytotoxic, e.g.,
XX anticancer drugs. Targeted delivery of such produg activators allows a
XX reduction in dose of the produg, and thus of systemic side-effects.
XX P450R derivative fusion proteins, or vectors that express them, are
XX specifically used to treat tumours, inflammation, atherosclerosis and
XX muscular dystrophy, but may also be used to treat many other conditions,
XX e.g., cerebral malaria, rheumatoid arthritis, or conditions associated
XX with hypoxia, ischaemia or hypoglycemia, or to deliver antibiotics,
XX antiviral agents, analgesics, anaesthetics, anti-inflammatories,
XX antineoplastic agents and diagnostic agents.

XX Sequence 301 AA:

Query Match 100.0%; Score 1561; DB 20; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.3e-122;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEDELYTPSSGMAASDPSPDTSRRGALOTRSRORGEVRFVY 60
DB 1 mtsrrsvksqprevpdeyedylytpssgmaspsdpdtsrrgalotrsrorgevrfvgy 60
QY 61 DESDVALYGGSSSEDEHPEVPTRRPVSGAVLSGPGPARAPPAGSGAGTPTTAPR 120
DB 61 desdvalyggsssedehpevprrtrpvsgavlspgparapppgsgaggtpttaptpr 120
QY 121 APPTORVATPAPAPAEETTRGRKSAOPESAAIPDAPASTAPRSTPAAGLARKLHFT 180
DB 121 apttrvattpapapaettrgrksaqpesaaipdpastaprcrsktpagglarklhft 180
QY 181 APPNDAPWTPRVAGFNKRVFCAVGLAAMHARMAAVQLMDSRPRTDEDLNELLGITT 240
DB 181 appndapwtprvagfnkrvfcaavglaaahmaavqldmsrptdedlnellgitt 240
QY 241 IRTVVEGKLLORANELVDPVVOVDATATRGSAASRPTEPRPARARSRRPRRY 300
DB 241 irtvvegkllqranelvdpvvovdatatrgsaasrpteprrpararsrrprpy 300
QY 301 E 301
DB 301 e 301

RESULT 2
AAV27404
ID AAV27404 standard: Protein: 301 AA.

XX AAV27404;

XX 23-NOV-1999 (first entry)

XX HSV-1 tegument protein VP22.

XX Produg; localization domain: tumor-selective antibody; cytochrome P450;

KW produg activating domain; modified hematopoietic stem cell; MHC; tumor;
KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; HSV; VP22;
KW tegument protein.

OS Herpes simplex virus type 1.

XX Key Location/Qualifiers
XX Region 251..267

FT /note="the corresponding DNA sequence for this region
FT is possibly missing; there are only 4 nucleotide
FT basepairs indicated as encoding for this entire
FT region"

W09945126-A2
10-SEP-1999

PF 05-MAR-1999; 99WO-GB00672.

XX 06-MAR-1998; 98GB-0004841.

PR 19-AUG-1998; 98GB-0018103.

PR 29-JAN-1999; 99GB-0002081.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths LJ;

XX Mitochondrion K;

DR WPI: 1999-540852/45.

DR N-PSDB: AA207807.

XX New produg activating agent targeted to selected cells or tissues,
XX particularly hypoxic cells, for treating e.g. tumors or inflammation -

XX Example 7; Fig 3d; 149pp: English.

XX The invention provides a new produg activating agent that comprises: (1)
XX a localization domain (LD); other than a tumor-selective antibody; and a
XX produg activating domain (PAD); (11) at least one nucleic acid encoding
XX a cytochrome P450 and under control of at least one constitutive or
XX inducible expression control sequence or (11) a modified hematopoietic
XX stem cell (MHC) containing at least one nucleic acid encoding a PAD and
XX under control of elements as in (11). The produg activating agent or
XX vectors that express them, are specifically used to treat tumors,
XX inflammation, atherosclerosis and muscular dystrophy, but may also be
XX used to treat many other conditions, e.g. cerebral malaria, rheumatoid
XX arthritis, or conditions associated with hypoxia, hypoglycemia or
XX ischemia, or to deliver antibiotics, antiviral agents, analgesics,
XX anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
XX agents. LD optimize activity of PAD, e.g. by delivering it to selected
XX locations or by delivering it to neighboring cells (bystander effect),
XX and allow a reduction in dose of produg, and thus of systemic side-
XX effects. Nucleic acids encoding the agent may be expressed selectively
XX in hypoxic cells. The present sequence represents the HSV-1 tegument
XX protein VP22. This is used in the construction of a fusion protein
XX comprising VP22 and a human P450 reductase derivative alp450R.

XX Sequence 301 AA:

Query Match 100.0%; Score 1561; DB 20; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.3e-122;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEDELYTPSSGMAASDPSPDTSRRGALOTRSRORGEVRFVY 60

DB 1 mtsrrsvksqprevpdeyedylytpssgmaspsdpdtsrrgalotrsrorgevrfvgy 60

QY 61 DESDVALYGGSSSEDEHPEVPTRRPVSGAVLSGPGPARAPPAGSGAGTPTTAPR 120

DB 61 desdvalyggsssedehpevprrtrpvsgavlspgparapppgsgaggtpttaptpr 120

QY	121	APRQROVATKAPAPRAAETTTGKRSAPESALPDAASTAPRPSKPRAGLARKHESF	180
Db	121	aprtqrvatkapaaraeettlgrtsaqpesaalpdapastaprtsktpagglarklhfst	180
QY	181	APPNDAPMTPRVAGFNKKRVFCAAVUGRLAAMHARMAAVQLMDMSRPTDEDLNELGITT	240
Db	181	appnpdpawprvqgfnktrvcaavugrlaamharmaavqlwmdsrptdeedlnellgitt	240
QY	241	IRATVCECKNLLQRANELVNPDVQVDVDAATATGKRSAAASPTERRAPAPARSRRPRPV	300
Db	241	lrvtwcecgknllqraanelvnpdvqvddaatatrtgsaaasprterpaprarsasrrprpv	300
QY	301	E 301	
Db	301	e 301	

XX	RESULT	3
XX	ID	AAB86329
XX		AAB86329 standard; Protein; 301 AA.
XX	AC	
XX		AAB86329;
DT		18-SEP-2001 (first entry)
XX		
DE		VP22 protein fragment.
XX		
KW	Fusion protein; VP22; E7; cell import signal; cell export signal; antigen; immunization; infection-induced auto-immune disease; tumor disease.	
XX		
OS	Unidentified.	
XX		
PN	WO200151516-A2.	
XX		
PD	19-JUL-2001.	
XX		
PF	15-JAN-2001; 2001WO-DE00134.	
XX		
PR	13-JAN-2000; 2000DE-1001230.	
XX		
PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.	
XX		
PI	Mueller M, Michel N, Osen W, Gissmann L, Zentgraf H;	
DR	WPI: 2001-442135/47.	
XX		
PT	Identifying an immunization agent comprising cell import and/or export signal sequences and an antigen for Immunizing against infection-induced auto-immune and tumor disease	
PS	Disclosure: Fig 4; 23pp; German.	
XX		
CC	This invention describes a fusion protein comprising cell import and/or export signal sequences and an antigen which is suitable for Immunizing an individual against a disease, together with a DNA that codes for said protein. The invention also relates to the use of the protein (II) and its encoding DNA (I) for Immunizing an individual against diseases, in particular against infection-induced auto-immune and tumor diseases. This sequence represents the VP22 protein fragment used in the construction of the fusion construct VP22-E7.	
XX		
XQ	Sequence	301 AA;

Query Match	100.0%	Score 1561;	DB 22;	Length 301;
Best Local Similarity	100.0%;	Pred. NO. 5.3e-122;		
Matches 301; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	MTSRSVKSGPREVPREDLYLTPSSGMASSPDSPDTSRRGAQOTRSRGRGEVAFVOY	60	
b	1	mtsrsvsgprvpredeydllytpssgmspsdpdtsrrgaqlttrsrgrevfivq	60	

Qy	61	DESUYALYCGSSSDDDHPEVPRRRRVSGAVLSCPEPAPAPPPPGSGAGCTPTTAPR	120
Db	61	desyalygssseddenpevprtrrrvsgavlsppapapppgag99agltptlapr	120
Qy	121	APRTORVATKPAAPAAETTRGRKSAOPESALPDAFASAPTRSKTPAGGLARKLHFST	180
Db	121	aprtqrvatkpeapaasettrgrksagpesaalpdapastaprctskcpagjarklhfsr	180
Qy	181	APPNPDAFWTRVAGFEMKRRVCAGVGLAMHARMMAVQLMDHSRPTDEDLNELLGITT	240
Db	181	appnpdapwtrvavgfmrkvfcaavgilaamharmaavqlwmdsrptdedlnellgilt	240
Qy	241	IRVVTCCEGKNLQRIANELVMPDVQDDAATATRGSRSAASRPTEPRAPARSAASRPRIY	300
Db	241	irvvccegnlqrianelvmpdvqvddaatatrgsraasrptcrpaprassrprpy	300
Qy	301	E 301	
Db	301	e 301	

XX	SEQUENCE	301 AA;
XX	DE	Herpes simplex viral protein: SEQ ID 26.
XX	DT	21-SEP-2001 (First entry)
XX	AC	AAG64275;
XX	ID	AAG64275 standard; protein; 301 AA.
XX	OS	Herpes simplex virus type 1.
XX	PN	W0200148014-A1.
XX	PD	05-JUL-2001.
XX	PF	26-DEC-2000; 2000WO-JP09274.
XX	PR	27-DEC-1999; 99JP-0371449.
XX	PA	(SHIO) SHIONOGI & CO LTD.
XX	PI	Shimizu S, Tsujimoto Y;
XX	DR	WPI; 2001-418246/44.
XX	PT	BH4-fused polypeptides with peptide sequences capable of exerting effect on enabling uptake into cells, applicable as effective apoptosis inhibitors, useful in preventives or remedies for ischemic diseases e.g. myocardial infarct
XX	PT	-
XX	PS	Claim 5; Page 74-6; 84pp; Japanese.
XX	CC	The present invention relates to BH4-fused polypeptides. The BH4-fused polypeptide have a sequence capable of affecting cellular uptake and also a BH4 domain sequence from an anti-apoptosis Bcl-2 family protein. The BH4-fused polypeptides are useful as effective apoptosis inhibitors, and are useful in preventives or remedies for ischemic diseases e.g. myocardial infarct, AIDS, neurodegenerative diseases, infective multiple failure, fulminant hepatitis and diabetes. The present peptide was used in the present invention.

Query Match	100.0%;	Score 1561;	DB 22;	Length 301;
Best Local Similarity	100.0%;	Pred. No. 5.3e-122;		

XX The present invention relates to use of fusion proteins comprising
 CC a site-specific DNA recombinase domain e.g. Cre and a protein
 CC transduction domain (PTD) e.g. the Human immunodeficiency virus
 CC (HIV) derived TAR peptide, for preparing an agent for inducing
 CC target gene alterations in a living organism or cell culture. The
 CC present invention also provides a method for inducing gene
 CC alterations in living organisms using the fusion proteins of the
 CC invention. The present sequence is VP22-P1pe fusion protein. The
 CC VP22 sequence is from Human spumaretrovirus (HSV).

XX Sequence 747 AA:

Query Match 100.0% Score 1561; DB 22; Length 747;

Best Local Similarity 100.0%; Pred. No. 1.6e-121; Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MTSRRSVKSGPREVPDEVEDLYTPSSGMA SPDSPPDTSRKGALQTRSRGGEVRFVQY 60
 |||
 1 mtsrrsvksqprevpdevedlytpssgmaspdsppdtsrrgaltqrsgvrfvgy 60
 QY 61 DESDVALYGGSSSEDDHEPVRTRRRPVSGAVLSCGPARAPP PPA GSGAGRTPTTAPR 120
 |||
 61 desdvalyggssseddhevpvtrrrpvsgavlsgpgrapppppgsgagrtptapr 120
 DB 121 APTQGVATKAPAAPAETTRGRKSAOPESALPDAPASTAPTRSKTPAOGIARKIHFTST 180
 |||
 121 aptqgvatkapaapaettrgrksaopsalpdapastaptrsktpaogiar kihftst 180
 QY 181 APPNDAPWTPPVAGFNKRVFCAVGRILAMHARMAAVOLMMSRPRTEDEINELIGIT 240
 |||
 181 appndapwtppvagfnkrfvcaavgrilaamhaavolwmmsrprtededineligit 240
 DB 241 IRTVCEGKNLQIRANELYNPDVODVDAATATRGSAASRPTERRAPARSASRRPRPV 300
 |||
 241 irtvcegnlqiranelynpdvovdvaatatrgrsaasrpterraparsasrrprpv 300
 QY 301 E 301
 |||
 301 e 301
 DB 301 e 301

RESULT 7

AAE05273 ID AAE05273 standard; Protein; 683 AA.

XX AC AAE05273;

DT 12-SEP-2001 (first entry)

DE VP22CreStreptag fusion protein.

XX DNA recombinase domain; protein transduction domain; PTD;
 KM VP22CreStreptag fusion protein; Human immunodeficiency virus; HIV;
 KM gene alteration; Human spumaretrovirus; HSV.

XX Chimeric - Human spumaretrovirus.

OS Chimeric - Unidentified.

PN WO200149832-A2.

XX 12-JUL-2001.

PF 05-JAN-2001; 2001WO-EP00060.

PR 07-JAN-2000; 2000EP-0100351.
 PR 10-NOV-2000; 2000EP-0124595.

XX (ARTE-) ARTEMIS PHARM GMBH.

XX Schwenk F;

DR WPI; 2001-441873/47.
 DR N-PSDB; AAD09268.

PT Using site-specific DNA recombinase domain/protein transduction domain
 PT fusion proteins for inducing target gene alterations in organisms or
 PT cell cultures -

PS Disclosure; Page 58-60; 85pp; English.

CC The present invention relates to use of fusion proteins comprising
 CC a site-specific DNA recombinase domain e.g. Cre and a protein
 CC transduction domain (PTD) e.g. the Human immunodeficiency virus
 CC (HIV) derived TAR peptide, for preparing an agent for inducing
 CC target gene alterations in a living organism or cell culture. The
 CC present invention also provides a method for inducing gene
 CC alterations in living organisms using the fusion proteins of the
 CC invention. The present sequence is VP22CreStreptag fusion protein.
 CC The VP22 sequence is from Human spumaretrovirus (HSV).

XX Sequence 683 AA:

Query Match 99.7% Score 1557; DB 22; Length 683;

Best Local Similarity 99.7%; Pred. No. 3.2e-121; Matches 300; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEVEDLYTPSSGMA SPDSPPDTSRKGALQTRSRGGEVRFVQY 60
 |||
 1 mtsrrsvksqprevpdevedlytpssgmaspdsppdtsrrgaltqrsgvrfvgy 60
 DB 61 DESDVALYGGSSSEDDHEPVRTRRRPVSGAVLSCGPARAPP PPA GSGAGRTPTTAPR 120
 |||
 61 desdvalyggssseddhevpvtrrrpvsgavlsgpgrapppppgsgagrtptapr 120
 QY 121 APTQGVATKAPAAPAETTRGRKSAOPESALPDAPASTAPTRSKTPAOGIARKIHFTST 180
 |||
 121 aptqgvatkapaapaettrgrksaopsalpdapastaptrsktpaogiar kihftst 180
 DB 181 APPNDAPWTPPVAGFNKRVFCAVGRILAMHARMAAVOLMMSRPRTEDEINELIGIT 240
 |||
 181 appndapwtppvagfnkrfvcaavgrilaamhaavolwmmsrprtededineligit 240
 QY 241 IRTVCEGKNLQIRANELYNPDVODVDAATATRGSAASRPTERRAPARSASRRPRPV 300
 |||
 241 irtvcegnlqiranelynpdvovdvaatatrgrsaasrpterraparsasrrprpv 300
 QY 301 E 301
 |||
 301 e 301
 DB 301 e 301

RESULT 8

AAW95099 ID AAW95099 standard; Protein; 301 AA.

XX AC AAW95099;

DT 25-MAY-1999 (first entry)

DE HIV-1 VP22 polypeptide.

XX Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
 KM CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KM intracellular; transcellular; transcytosis; vascular wound; repair; hair;
 KM smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
 KM cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KM tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 KM tachycardia; HIV-1.

XX Human immunodeficiency virus type 1.

XX WO9906540-A2.

PD 11-FEB-1999.
XX
XX
PF 29-JUL-1998: 98WO-US151759.
XX
XX 29-JUL-1997: 97US-0902572.
XX
XX (MITO-) MITOTIX INC.
XX
XX Beach DH, Gyuris J, Lamphere L;
XX
XX MPI: 1999-153770/13.
DR N-PSDB: AAX26227.
XX
XX Fusion and chimaeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
XX
XX Example 2; Page 26-27; 88pp; English.
PS
XX The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a
CC CDK, linked to a transcription regulator functional in eukaryotic cells;
CC (ii) second gene construct comprising a sequence encoding a polypeptide
CC that promotes endothelialisation, and (iii) a gene delivery composition
CC for delivering the GCs to a cell for transfection. Also provided are
CC nucleic acids encoding a fusion protein (FP) containing: (i) a
CC therapeutic polypeptide sequence (TP) from an intracellular protein that
CC alters a cellular process when FP enters the cell, and (ii) a
CC transcellular polypeptide sequence (TCP) that promotes transcytosis of
CC FP. The FP consists of at least one CDK-binding motif and a TCP. See
CC AAX26220 for detailed uses of the recombinant transfection system. The
CC CKI polypeptides are engineered to include any of the peptides shown in
CC AAW5097-100 encoded by the DNA sequences AAX26225-228.
XX
SQ Sequence 301 AA:

Query Match 99.6%; Score 1554; DB 20; Length 301;
Best Local Similarity 99.7%; Pred. No. 2e-121;
Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEYEDLYTPSSGMASSPDSPDTSRRGALOTRSRQGEVRFVQY 60
DB 1 mtsrrsvksgprevpdeyedlytpssgmaspsdpdtsrrgalotrsrqgevrivgy 60
QY 61 DESDYALYGGSSSEDEHPEVPTRRPVSGAVLSGPGPARAPPPAGSGAGRTPTTAPR 120
DB 61 desdyalygsssedehpevprrtrpvsgavlspgparappppagsgagrtpttapt 120
QY 121 APRTQVATKAPAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAGLARKLHFST 180
DB 121 aptqvatkapaapaettrgrksaqpesaalpdapastapttrsktpaglarlkhfst 180
QY 181 APPNPDAWTPRVAGFNKRFCAAVGRLAAMHARMAAVOLMDMSRPTDDLDELIGITT 240
DB 181 appnpdawtprvagfnkrfcaavgrlaamharmaaavqlwdmsrptdedlneilgilt 240
QY 241 IRTVTCGKLLQRLANELVNPVQDVDAATATGRSAASRPTERRPARASASRRPRPV 300
DB 241 irtvtcgkllqrlanelvnpdvqddaataatgrsaasrpterrparasasrrprpv 300
QY 301 E 301
DB 301 e 301

RESULT 9
AAV79877
ID AAV79877 standard; Peptide: 301 AA.

XX
XX AAV79877;
AC
XX
XX 10-MAY-2000 (first entry)
DT
XX
XX HSV-1 VP22 peptide.
DE
XX
XX Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic;
KW E1; antiviral; virucide; cytostatic; antiproliferative; dermatological;
KW preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart;
KW epidermodysplasia verruciformis; anorectal carcinoma.
XX
XX Herpes simplex virus type 1.
OS
XX
XX WO200001720-A2.
PN
XX
XX 13-JAN-2000.
PD
XX
XX 02-JUL-1999: 99WO-US15144.
PF
XX
XX 02-JUL-1998: 98US-0091661.
PR
XX
XX (HARD) HARVARD COLLEGE.
PA
XX
XX Howley P, Benson J, Kasukawa H;
PI
XX
XX MPI: 2000-171001/15.
DR N-PSDB: AAZ88468.
DR
XX
XX use of papillomavirus E2 protein peptidomimetics for treating
PT papillomavirus-infected cells and papillomavirus-induced conditions in
PT mammals by inhibiting E1-E2 interaction
PS
XX
XX Disclosure; Page 42; 110pp; English.
PS
XX
XX The present invention describes the use of a small organic compound (A)
CC which competitively inhibits interaction of a papillomavirus (PV) E2
CC protein with a PV E1 protein for treating a cell infected with PV or a
CC mammal with a PV-induced condition. (A) has antiviral, virucide,
CC cytostatic, antiproliferative and dermatological activities. Methods
CC from the present invention can be used to treat PV-induced conditions
CC including growth of PV preneoplastic and neoplastic lesions, cutaneous
CC lesions chosen from warts and other benign cutaneous lesions, planter
CC warts (verruca plantaris), common warts (verruca plana), Butcher's
CC common warts, flat warts, genital warts (condyloma acuminatum) and
CC epidermodysplasia verruciformis, laryngeal, oral, pharyngeal,
CC oesophageal and other upper airway papilloma or vaginal, cervical,
CC vulvar, penile and anorectal carcinoma. The E2 inhibitors may also be
CC used to treat epithelial and internal fibropapillomas in animals.
CC The present sequence represents a peptide sequence used in the
CC exemplification of the present invention.
XX
SQ Sequence 301 AA:

Query Match 99.6%; Score 1554; DB 21; Length 301;
Best Local Similarity 99.7%; Pred. No. 2e-121;
Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEYEDLYTPSSGMASSPDSPDTSRRGALOTRSRQGEVRFVQY 60
DB 1 mtsrrsvksgprevpdeyedlytpssgmaspsdpdtsrrgalotrsrqgevrivgy 60
QY 61 DESDYALYGGSSSEDEHPEVPTRRPVSGAVLSGPGPARAPPPAGSGAGRTPTTAPR 120
DB 61 desdyalygsssedehpevprrtrpvsgavlspgparappppagsgagrtpttapt 120
QY 121 APRTQVATKAPAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAGLARKLHFST 180
DB 121 aptqvatkapaapaettrgrksaqpesaalpdapastapttrsktpaglarlkhfst 180
QY 181 APPNPDAWTPRVAGFNKRFCAAVGRLAAMHARMAAVOLMDMSRPTDDLDELIGITT 240
DB 181 appnpdawtprvagfnkrfcaavgrlaamharmaaavqlwdmsrptdedlneilgilt 240

Db 181 appndapwlpvrgfinkrfvicaavgrlaamharmavqlwdmsrptdcdlnellgltt 240
 QY 241 IRTVCEGKNTLQRANELVNPVDVDAATATRGSAASRPTERRAPARSASRRPRV 300
 Db 241 IRTVCEGKNTLQRANELVNPVDVDAATATRGSAASRPTERRAPARSASRRPRV 300
 QY 301 E 301
 Db 301 e 301

RESULT 10
 AAB60910 ID AAB60910 standard; Protein; 301 AA.
 AAB60910; 05-NOV-2001 (first entry)
 DE HSV-1 VP22 protein.
 KW Co-activator domain; P300/CBP KIX domain; erythrocythemia; skin disease;
 KW polycythemia; haemoglobinopathy; cell differentiation; ulcer; cancer;
 KW neurological condition; neurodegenerative disease; immune disease;
 KW diabetes.
 OS Synthetic.
 PN WO200118036-A2.
 PD 15-MAR-2001.
 PF 31-AUG-2000; 2000WO-US24010.
 PR 03-SEP-1999; 99US-0152402.
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA (JOSL-) JOSLIN DIABETES CENT.
 PI Frangioni JV, Cantley LC, Montminy MR;
 DR WPI; 2001-273380/28.
 DR N-PSDB; AAF58996.
 XX Identifying co-activator domain specific transcriptional activators by
 PT contacting a target domain of a selected transcription factor with a
 PT peptide display library, where the identified binding peptides are
 PT useful for reducing hyperglycemia -
 PS Disclosure; Page 78; 156pp; English.
 CC The present invention describes a method of identifying the co-activator
 CC domain of specific synthetic activators, involving contacting the target
 CC domain of a selected transcription factor with a peptide display library,
 CC and identifying those sequences which bind to the target domain. In
 CC particular, those which bind to the KIX domain of P300/CBP are useful.
 CC The peptides can be used in the treatment of diseases related to aberrant
 CC KIX-dependent gene transcription, including erythrocythemia,
 CC polycythemia, haemoglobinopathies, to regulate cell differentiation, to
 CC treat neurological diseases, immunological diseases, diabetes, ulcers,
 CC skin diseases and cancer, and to aid wound healing. The present sequence
 CC is a protein described in the exemplification of the invention.
 CC XX
 SQ Sequence 301 AA;

Query Match 99.6%; Score 1554; DB 22; Length 301;
 Best Local Similarity 99.7%; Pred. NO. 2e-121;
 Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSRSVSGPREVREDYEDLYTPSSGMASSPDPSTRGALQTRSRQGEVRFVQY 60
 Db 1 mtsrsvsgprevedyedytpssgmaspsdpdstrrgalqtrsrqgevrivgy 60

QY 61 DESDVALYCGSSSEDDHEPVRPRPVSGAVLSGPPAPAPPPAGSGAGRTPTTAPR 120
 Db 61 desdvalyggssseddehpvrtrpvsavlsppgparepppagsgagrtpttapr 120
 QY 121 APPRTQVATKAPAAPAERTTRGRKSAOESALPDAPASTAPTSKPTPAOGLAKLFST 180
 Db 121 aptqrvatkapaapaeerttrgrksaopesalpdapastaptskptpaoglarklfst 180
 QY 181 APPNDAPWLPVRYAGNKKVFCAGRLAAMHARMAAVOLMDMSRPTDDEJNELLGIT 240
 Db 181 appndapwlpvryagfinkrfvicaavgrlaamharmavqlwdmsrptdcdlnellgltt 240
 QY 241 IRTVCEGKNTLQRANELVNPVDVDAATATRGSAASRPTERRAPARSASRRPRV 300
 Db 241 IRTVCEGKNTLQRANELVNPVDVDAATATRGSAASRPTERRAPARSASRRPRV 300
 QY 301 E 301
 Db 301 e 301

RESULT 11
 AAM47194 ID AAM47194 standard; Protein; 301 AA.
 AAM47194; 03-JUL-1998 (first entry)

DE Herpes simplex virus tegument protein VP22.
 KW Herpes tegument protein; VP22; UL49; antiviral agent; treatment;
 KW cold sore; genital herpes; chickenpox; shingles.
 OS Herpes simplex virus.
 PN WO9804708-A1.
 PD 05-FEB-1998.
 PF 28-JUL-1997; 97WO-GB02036.
 PR 26-JUL-1996; 96GB-0015726.
 PA (MEDI-) MEDICAL RES COUNCIL.
 PI Hope RG, McGeoch DJ, McLaughlan J, Rixon HM;
 DR WPI; 1998-130696/12.
 DR N-PSDB; AAV17085.
 XX New antiviral agent disrupting binding of VP22 to VP16 or gB -
 PT useful for treating infections caused by herpes simplex, e.g. cold
 PT sores and chicken-pox
 PS Example; Pages 49-50; 75pp; English.
 CC The present sequence is the herpes simplex virus (HSV)
 CC tegument protein VP22. VP22 was used in the preparation of a novel
 CC antiviral agent, which inhibits the maturation and/or replication
 CC of HSV by disrupting association between VP22 and VP16 and/or gB.
 CC The agent can be used to treat, e.g. cold sores, genital herpes,
 CC chickenpox and shingles.
 CC XX
 SQ Sequence 301 AA;

Query Match 99.5%; Score 1553; DB 19; Length 301;
 Best Local Similarity 99.7%; Pred. NO. 2.5e-121;
 Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSRSVSGPREVREDYEDLYTPSSGMASSPDPSTRGALQTRSRQGEVRFVQY 60
 Db 1 mtsrsvsgprevedyedytpssgmaspsdpdstrrgalqtrsrqgevrivgy 60

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Db 1 mtsrsvksqpreyprdeyedylytspsgmaspdpdtsrrgalqtrsrqgevrftvy 60
QY 61 DESDVALYGGSSSEDEHPEVPRTRRPVSGAVLSGPGPARAPPAGSGAGRTPTTAPR 120
Db 61 desdyalygssseddehpvprtrtrpvsavlsqpgparpppagsgagrtptapr 120
QY 121 APRQVATKAPAAPAAETTRGRKSAQPEASALPDAPASTAPTRSKTPAOGIARKLHFS 180
Db 121 aprtrvatckapaaettrgrksaqpesaalpdapastaptrsktpaqglarklhfst 180
QY 181 APPNDAPWTPRVAGFNKRVFCAGVGLAAMHARMAAVQLMDMSRPTDEDNELLGITTT 240
Db 181 appndapwtprvagfnkrfvcaavgrlaamharmavqlmdmsrptdednellgltt 240
QY 241 IRYTVCEGKNLLQANELVNPVDVDAATATGRSAASRPTERRAPARASARRRPV 300
Db 241 lrvtvcegknllqanelvnpdvqvdacatatrgrsaasrpterraparsarrpvp 300
QY 301 E 301
Db 301 e 301

```

RESULT 12

AAV83261 ID AAV83261 standard; Protein: 301 AA.

AAV83261: XX

DT 16-AUG-2000 (first entry)

DE HSV-1 V22 cellular localisation signal sequence.

KW Ubiquitin ligase; SCF; F-box protein; targeted degradation;

KM destabilisation; proteolysis; drug discovery; gene therapy; cancer;

OS Synthetic.

PN WO200022110-A2.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US23705.

PR 09-OCT-1998; 98US-0103787.

PA (HARD) HARVARD COLLEGE.

PI Zhou P, Howley P;

DR WPI: 2000-317970/27.

DR N-PSDB: AA293717.

PT Targeting degradation of polypeptide useful for treating cancer and

PS other proliferative disorders, involves conjugating polypeptide with

XX compound

XX Disclosure: Page 76; 185pp; English.

CC The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin

CC ligases) which can be used for the targeted degradation of a target

CC polypeptide in vivo. Targeted degradation is achieved by expressing

CC the ubiquitin ligase in a cell linked to the interaction domain of

CC the target polypeptide and thereby recruiting the target polypeptide

CC to the ubiquitin ligase. Such methods are useful for decreasing or

CC increasing the level of a target polypeptide and for creating and

CC expressing a destabilized polypeptide which is subjected to SCF

CC mediated proteolysis. Degrading any desired protein in a cell is

CC useful for preventing or treating diseases caused by the presence of

CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal. The hybrid ubiquitin ligase may also include an
 CC optional localisation sequence such as this HSV-1 V22 sequence.

SQ Sequence 301 AA;

Query Match

Best Local Similarity 99.7%; Score 1553; DB 21; Length 301;

Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MTSRSVKSQPREYPRDEYEDLYTTPSSGMA SPDPDTSRRGALQTRSRQGEVRFYQ 60
Db 1 mtsrsvksqpreyprdeyedylytspsgmaspdpdtsrrgalqtrsrqgevrftvy 60
QY 61 DESDVALYGGSSSEDEHPEVPRTRRPVSGAVLSGPGPARAPPAGSGAGRTPTTAPR 120
Db 61 desdyalygssseddehpvprtrtrpvsavlsqpgparpppagsgagrtptapr 120
QY 121 APRQVATKAPAAPAAETTRGRKSAQPEASALPDAPASTAPTRSKTPAOGIARKLHFS 180
Db 121 aprtrvatckapaaettrgrksaqpesaalpdapastaptrsktpaqglarklhfst 180
QY 181 APPNDAPWTPRVAGFNKRVFCAGVGLAAMHARMAAVQLMDMSRPTDEDNELLGITTT 240
Db 181 appndapwtprvagfnkrfvcaavgrlaamharmavqlmdmsrptdednellgltt 240
QY 241 IRYTVCEGKNLLQANELVNPVDVDAATATGRSAASRPTERRAPARASARRRPV 300
Db 241 lrvtvcegknllqanelvnpdvqvdacatatrgrsaasrpterraparsarrpvp 300
QY 301 E 301
Db 301 e 301

```

RESULT 13

AAV96574 ID AAV96574 standard; Protein: 297 AA.

AAV96574: XX

DT 12-SEP-2000 (first entry)

DE HSV-1 VP22 polypeptide.

KW hEST2; telomerase; catalytic subunit; reverse transcriptase; 11fe-span;

KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;

KW INK4; HSV-1; VP22; fusion protein.

OS Herpes simplex virus 1.

PN WO200031238-A2.

PD 02-JUN-2000.

PF 24-NOV-1999; 99WO-US27907.

PR 25-NOV-1998; 98US-0109891.

PR 17-FEB-1999; 99US-0120549.

PA (GENE-) GENETICA INC.

PI Hannon GJ, Beach DH;

DR WPI: 2000-400055/34.

DR N-PSDB: AAA29395.

XX New method for increasing the proliferative capacity of cell lines
 PT comprises administering agents reversibly activating telomerase
 PT activity and reversibly inactivating Rb/INK4 and/or p53 pathways useful
 PT in treating age related diseases

XX Disclosure: Page 31-32; 123pp; English.

XX The HSV-1 VP22 polypeptide can be fused to a retinoblastoma (Rb)
 CC inactivator protein sequence to aid targeting and internalization.
 CC The invention concerns methods and reagents for extending the life-span,
 CC e.g. the number of mitotic divisions, of a cell. The method relies on
 CC activation of a telomerase activity and inhibition of one or both of a
 CC Rb/INK4 pathway or a p53 pathway. Phosphorylation of Rb by
 CC cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the
 CC division cycle. Binding of INK4 family members, e.g. the tumour
 CC suppressor p16INK4a, inhibits kinase activity and results in growth
 CC arrest. Rb inactivators can selectively and reversibly inactivate an
 CC Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2
 CC is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor
 CC and can also be used in the methods. Other molecules which can be used
 CC include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
 CC differs from at one or more of residues K22, R24, H95 and/or D97.
 CC Additional constructs include a papilloma virus E7 protein, or other
 CC viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
 CC the Rb and p16INK4a genes may also be used. The methods are useful for
 CC increasing the proliferative capacity of cells. The cells are
 CC subsequently of use in pharmaceutical and cosmetic preparations used to
 CC treat conditions related to (premature) ageing, e.g. macular degeneration
 CC and arteriosclerosis. The cells can also be used to replace tumour cell
 CC lines in vitro and for studies on biochemical and physiological aspects
 CC of growth and differentiation. Long lived (immortal) cells could also be
 CC of use in the production of normal or genetically engineered
 CC biotechnology products.

XX Sequence 297 AA:

Query Match 97.4%; Score 1520; DB 21; Length 297;
 Best Local Similarity 98.3%; Pred. No. 1.4e-118;
 Matches 296; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 MTSRSVSGPREVREDEYEDLYTPSSGMA SPDSPPTSRGALQTRSGRGEVRFYQY 60
 DB 1 mtsrsvsgprevr-----dlytpssgmaspdspptsrgrgalqtrsggrvrfyqy 56
 QY 61 DESDYALYGSSSEDEHPEVPRTRRPVSGAVLSGPPARAPPPAGSGGAGRTPTTAPR 120
 DB 57 desdyalygsssedehpevprtrrtrrpvsgavlsppparappppagsggagrtpttpr 116
 QY 121 APRORVATKAPAAPAETTRGRKSAOPESALPDAPASTATRSKTPAOGIARKLHST 180
 DB 117 aprtrvatkapaapaettrgrksaopesaalpdpastatrtsktpragiarlkhst 176
 QY 181 APNPDAWTPPVAGFNKRVFCAVGRLAAMHARMAAVALMDMSRPDEDNELIGITTT 240
 DB 177 appnpdwpvtrpvagfnkrfvcaavgrlaamharmaaavqlwmsprdednelignlgtt 236
 QY 241 IRVTVCEGKNLIQRANELVNPVDVDAATATRGSAASRPTERRAPARSASRRPRPV 300
 DB 237 lrvtvcgknllqretelvpnpvqvdvdaatatrgrsaasrpterraparsasrrprpv 296
 QY 301 E 301
 DB 297 e 297

RESULT 14
 AAB86330
 ID AAB86330 standard; Protein: 267 AA.
 XX AAB86330;
 AC
 XX

DT 18-SEP-2001 (first entry)
 XX VP22 protein fragment VP22deltaC.
 DE

XX Fusion protein: VP22; E7; cell import signal; cell export signal;
 KW antigen; immunization; infection-induced auto-immune disease;
 KW tumor disease.

XX Unidentified.

XX WO200151516-A2.

XX 19-JUL-2001.

XX 15-JAN-2001; 2001WO-DE00134.

XX 13-JAN-2000; 2000DE-1001230.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Mueller M, Michel N, Osen W, Gissmann L, Zentgraf H;
 DR WPI: 2001-442135/47.

PT Identifying an immunization agent comprising cell import and/or
 PT export signal sequences and an antigen for immunizing against
 PT infection-induced auto-immune and tumor disease

XX Disclosure: Fig 4; 23pp; German.

XX This invention describes a fusion protein comprising cell import and/or
 CC export signal sequences and an antigen which is suitable for immunizing
 CC an individual against a disease, together with a DNA that codes for said
 CC protein. The invention also relates to the use of the protein (II) and
 CC its encoding DNA (I) for immunizing an individual against diseases. In
 CC particular against infection-induced auto-immune and tumor diseases. In
 CC sequence represents the VP22 protein fragment VP22deltaC used in the
 CC construction of the fusion constructs described in the method of the
 CC invention.

XX Sequence 267 AA:

Query Match 89.2%; Score 1392; DB 22; Length 267;
 Best Local Similarity 100.0%; Pred. No. 5.4e-108;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRSVSGPREVREDEYEDLYTPSSGMA SPDSPPTSRGALQTRSGRGEVRFYQY 60
 DB 1 mtsrsvsgprevr-----dlytpssgmaspdspptsrgrgalqtrsggrvrfyqy 60
 QY 61 DESDYALYGSSSEDEHPEVPRTRRPVSGAVLSGPPARAPPPAGSGGAGRTPTTAPR 120
 DB 61 desdyalygsssedehpevprtrrtrrpvsgavlsppparappppagsggagrtpttpr 120
 QY 121 APRORVATKAPAAPAETTRGRKSAOPESALPDAPASTATRSKTPAOGIARKLHST 180
 DB 121 aprtrvatkapaapaettrgrksaopesaalpdpastatrtsktpragiarlkhst 180
 QY 181 APNPDAWTPPVAGFNKRVFCAVGRLAAMHARMAAVALMDMSRPDEDNELIGITTT 240
 DB 177 appnpdwpvtrpvagfnkrfvcaavgrlaamharmaaavqlwmsprdednelignlgtt 240
 QY 241 IRVTVCEGKNLIQRANELVNPVDVDAATATRGSAASRPTERRAPARSASRRPRPV 300
 DB 241 lrvtvcgknllqretelvpnpvqvdvdaatatrgrsaasrpterraparsasrrprpv 296

RESULT 15
 AA78333
 ID AA78333 standard; peptide: 246 AA.
 XX AA78333;
 AC

XX 04-MAY-2000 (first entry)
DT
XX

DE Herpes simplex virus VP22 protein SEQ ID NO:5.
XX

KW Cell membrane permeant; medical imaging; diagnosis; radiotherapy;
pharmaceutical therapy; drug delivery.
XX

OS Herpes simplex virus.
XX

PN WO967284-A2.
XX

PD 29-DEC-1999.
XX

PF 18-JUN-1999; 99WO-US13660.
XX

PR 20-JUN-1998; 98US-0090087.
XX

PA (UNITW) UNIV WASHINGTON.
XX

PI Plvnicia-Worms D;
XX

DR WPI: 2000-160576/14.
XX

PT New membrane permeant peptide complexes for medical imaging,
diagnostics and therapy
XX

PS Claim 3; Page 17; 65pp; English.
XX

CC The present invention describes compound comprising a cell membrane
permeant peptide, a diagnostic or an active substance and a functional
linker moiety linking them, where the functional linker moiety confers
target cell specificity to the compound or a salt of the compound. The
CC compounds and compositions are useful in the fields of medical imaging,
diagnostics and pharmaceutical therapy. The composition are for medical
CC imaging, evaluating intracellular processes, radiotherapy of
intracellular targets and drug delivery. The cell membrane permeant
CC peptides conjugate coordination and covalent complexes have target cell
specificity, therefore, the Tat peptide and other cell membrane permeant
CC peptides can be used to selectively deliver non- or poorly permeant
drugs, diagnostic substances such as oligonucleotides, peptides, peptide
CC nucleic acids, fluorochromes, dyes, enzyme substrates and metals useful
in medical therapy, imaging and/or diagnostics selectively to cells
CC in vivo only when functional linkers are introduced into permeant peptide
CC constructs. The present sequence represents a specifically claimed
cell membrane permeant peptide from the present invention.

CC
XX
SQ Sequence 246 AA:

Query Match 77.1%; Score 1203.5; DB 21; Length 246;
Best Local Similarity 80.7%; Pred. No. 2,4e-92;
Matches 243; Conservative 0; Mismatches 3; Indels 55; Gaps 2;

OY 1 MTSRSKVGKSGPRVPRDEDELYTTPSSGMAFSDSPPTSRKALOTRSRQGEVRFVQY 60
|||||
DB 1 MTSRSKVGKSGPRVPRDEDELYTTPSSGMAFSDSPPTSRKALOTRSRQGEVRFVQY 60
OY 61 DESDVALYCGSSSEDEHPEVPRTRRRVSGAVLSCGPARAPPPAGSGAGRTPTAPR 120
|||||
DB 61 desdvalyggsssedehpevprtrrrvsgavlsqpparapppagsgagrtptapt 120
OY 121 APPRQVATKAPAPAAETTRGRKSAQPSAALPDAFASTAPTFRSKTPAQLARKLHFTST 180
|||||
DB 121 aprtqrvaekapapaettrgrksaqpsaalpdastapt----- 163
OY 181 APPNPDPAPTPRVAGFNKRVFCAVGRLLAAMARMAVOLMDKSRPRTDEDLNELIGITT 240
|||||
DB 164 -----vqlwmsrptdedlnellgltth 186
OY 241 IRVTGCEGNLORANELYNPDVVDVDAATATRGSAASRPTERRAPARASASRRRPV 300
|||||
DB 187 -rvlvcegnllqranelvnpdvvdvdaatatrgrsaasrpterraparsasrrprpv 245

OY 301 E 301
DB 246 e 246

Search completed: August 28, 2002, 12:23:40
Job time: 324 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:20:31 ; Search time 17.53 Seconds
(without alignments)
1649.908 Million cell updates/sec

Title: US-09-522-278b-12

Sequence: 1 MTSRRSVKSGPREVPDEYE.....PTERRAPARASAPRRPVE 301

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1561	100.0	301	1 WMBEP9	UL49 protein - hum
2	303	19.4	304	1 WZBEA9	33.2K tegument pro
3	270.5	17.3	290	2 S36706	B4 protein - equin
4	270.5	17.3	304	2 T42554	tegument protein -
5	245.5	15.7	195	2 S24228	BH7-1 protein homo
6	225.5	14.4	302	1 WZBE9	gene 9 protein - h
7	211	13.5	249	2 S60741	major tegument pro
8	210	13.5	249	2 JQ2201	UL49h protein - Ma
9	161.5	10.3	1460	1 EDBE1F	BH1F1 protein - hu
10	161	10.3	1460	1 EDBE1F	immediate-early pr
11	153.5	9.8	1446	1 A45344	glycoprotein A - m
12	149	9.5	846	2 S52318	hypothetical prote
13	146.5	9.4	395	2 H75457	hypothetical prote
14	146	9.4	839	2 F75518	hypothetical prote
15	144	9.2	1037	2 B87254	translational initia
16	144	9.2	1201	2 G86441	unknown protein (i
17	140.5	9.0	1282	2 J80120	glycoprotein A - m
18	140.5	9.0	1952	2 T48814	hypothetical prote
19	140	9.0	1132	2 C75255	probable iron-sulf
20	139.5	8.9	932	2 T21338	hypothetical prote
21	139	8.9	438	1 WMBE38	arylesterase-relat
22	138	8.8	358	1 WMBE38	infected cell prot
23	137	8.8	590	1 T35297	probable dihydrol
24	137	8.8	1069	2 S27922	nuclear antigen EB
25	136.5	8.7	1320	2 JCS630	TCOF1 protein - mo
26	135.5	8.7	754	2 B97586	hypothetical prote
27	135.5	8.7	754	2 AC2807	Ompa family protei
28	135	8.6	261	1 WMBEXE	infected cell prot
29	134.5	8.6	3149	1 QOBE8	BpF1 protein - hu

30	134	8.6	2187	2 T30826	nascent polypeptid
31	130	8.3	507	2 T44768	antifreeze glycope
32	130	8.3	858	2 S15762	neurofilament trip
33	129.5	8.3	550	2 C75557	hypothetical prote
34	129.5	8.3	901	2 A49227	sialidase - Actino
35	129	8.3	375	2 T08134	oleosin-like prote
36	129	8.3	509	2 T34871	probable membrane
37	128	8.2	725	2 T33498	hypothetical prote
38	128	8.2	2022	2 T48818	glucan 1,4-alpha-g
39	127.5	8.2	608	2 A35021	myosin-light-chain
40	127.5	8.2	822	2 T51049	related to nucleol
41	127	8.1	1791	2 T02345	hypothetical prote
42	127	8.1	3164	1 WMBE6	U136 protein - hum
43	126.5	8.1	476	2 T27051	hypothetical prote
44	126.5	8.1	628	2 J00110	hypothetical 69k p
45	126.5	8.1	801	2 T29018	hypothetical prote

ALIGNMENTS

RESULT 1	
WMBE9	
UL49 protein - human herpesvirus 1 (strain 17)	
C:Species: human herpesvirus 1	
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000	
C:Accession: D30089	
R:McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P	
J. Gen. Virol. 69, 1531-1574, 1988	
A:Title: The complete DNA sequence of the long unique region in the genome of herpes	
A:Reference number: A30083; MUID:88274327	
A:Accession: D30089	
A>Status: nucleic acid sequence not shown; translation not shown	
A:Molecule type: DNA	
A:Residues: 1-301 <MCG>	
A:Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32299.1; PID:g59549; GB:D00317	
A:Genetics:	
A:Gene: UL49	
C:Superfamily: varicella-zoster virus gene 9 protein	
Query Match	100.0%; Score 1561; DB 1; Length 301;
Best Local Similarity	100.0%; Pred. No. 6.4e-86;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MTSRRSVKSGPREVPDEYEDLYTPSSGMA SPDSPTSRGALQTRSGRGEVRFVQY 60	
DB 1 MTSRRSVKSGPREVPDEYEDLYTPSSGMA SPDSPTSRGALQTRSGRGEVRFVQY 60	
QY 61 DESDVALYGGSSSEDDHEPVRTRRPVSGAVLSGPGARAPPPAGSGAGRTPTTAPR 120	
DB 61 DESDVALYGGSSSEDDHEPVRTRRPVSGAVLSGPGARAPPPAGSGAGRTPTTAPR 120	
QY 121 APTGQVATKAPAAEAETTRGRKSAOPESALPPAPASTATRTSKTPAGCLARKLHFT 180	
DB 121 APTGQVATKAPAAEAETTRGRKSAOPESALPPAPASTATRTSKTPAGCLARKLHFT 180	
QY 181 APTGQVATKAPAAEAETTRGRKSAOPESALPPAPASTATRTSKTPAGCLARKLHFT 240	
DB 181 APTGQVATKAPAAEAETTRGRKSAOPESALPPAPASTATRTSKTPAGCLARKLHFT 240	
QY 241 IRVTTCCEGKNLLORANELVNPVDVDAATATTRGRSAASRTTERPARAPASAPRRPV 300	
DB 241 IRVTTCCEGKNLLORANELVNPVDVDAATATTRGRSAASRTTERPARAPASAPRRPV 300	
QY 301 E 301	
DB 301 E 301	
RESULT 2	
WZBEA9	
33.2K tegument protein - equine herpesvirus 1 (strain Ab4p)	

C:Species: equine herpesvirus 1
A:Note: host Equus caballus (domestic horse)
C:Date: 30-Sep-1992 #sequence_rev1sion 30-Sep-1992 #text_change 16-Jul-1999
C:Accession: C36796
R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Submitted to Genbank, March 1992
A:Description: The DNA sequence of equine herpesvirus-1.
A:Reference number: A36805
A:Accession: C36796
A:Molecule type: DNA
A:Residues: 1-304 <TEL>
A:Cross-references: GB:88664; NID:q330791; PIDN:AA802446.1; PID:q330803
R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A:Title: The DNA sequence of equine herpesvirus-1.
A:Reference number: A41831; MID:9229556
A:Contents: annotation: possible protein-coding frames
A:Note: neither amino acid nor nucleotide sequence is given
C:Genetics:
A:Gene: 11
C:Superfamily: varicella-zoster virus gene 9 protein

Query Match	19.4%	Score 303	DB 1	Length 304
Best Local Similarity	32.4%	Pred. No. 2,6e-11		
Matches	93	Conservative	30	Mismatches 96
			Indels	68
			Gaps	11
QY	21	DLYTPSSGMSAPDPSPTSRGALQTRSKORGEVNO-----YDESDYALGSSS	73	
Db	58	DLYES-----ASPNDKKVYTRRG-MSTAAYHDSSEHITYETCGDEYDACEVSLIG---	108	
QY	74	EDDEHPVEVPRTRRPVSGAVLSCPG---PARAPPPPAGSCGAGRTPTTAPRAVTRTORVATK	130	
Db	109	-----GKLTSTNGNSQSPAKKAPPPRGAAA---PPRVYTRRPTTAAAT-	149	
QY	131	APAAPAELTRGRKSKAOPESAALPDPAAPASTAFTRSKTPAGCLARKLHSTAPPNDAAPT	190	
Db	150	-----STTPPOQCCAPKQASPG-----VNSTSKSGGLA---FSGTRKTPPSQY	191	
QY	191	PRVAGFNKRVFCAAGRLMAHARMAAAVOLMMSRPRTDEDLNELGITITVTCCEGKN	250	
Db	192	GATHLFNNKVFCAAVSRVAANAASDAASALMDLNPRTKTEDDLRFKAANAIRLVCEGAQ	251	
QY	251	LLQGRANELVNPVDVDAATATGRGSAASRPTERRAARASASRR	297	
Db	252	LLGVANSTVE-----STPDGYAAGGNGYDRRP-KTASRR	286	

RESULT 3
S36706
B4 protein - equine herpesvirus 4
C:Species: equine herpesvirus 4
C:Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 20-Jun-2000
C:Accession: S36706
R:Rigolo, P.
submitted to the EMBL Data Library, November 1989
A:Reference number: S36703
A:Accession: S36706
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <RIG>
A:Cross-references: EMBL:X17684; NID:q2578026; PIDN:CAA35674.1; PID:q2578022
C:Superfamily: varicella-zoster virus gene 9 protein

Query Match	17.3%	Score 270.5	DB 2	Length 290
Best Local Similarity	34.4%	Pred. No. 2	1e-09	
Matches	85	Conservative	18	Mismatches 77; Indels 67; Gaps 11
Qy	60	VDSDYALTCGSSSEDDHEVPRTRRPVSGAVLSPG---	PARAPPPAGSGGAGRTPT	116
Db	84	YDACETSLVGG-----GKLTSTSHGLSLPTKTTNPK---	SAACVPT	120

— 9 —

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OY 117 TAPRPFQPVATKAPARALETTRGKSKAPESASALPDPAPASAPTRSTPAQGL-AR 174
Db 121 -----PQRV-----PARPA-----RAAP--SATPTQPCVAKRSTSPGNSIKSK 161
OY 175 KLHESAPNDAPWTPRVAGFNKRVFCAAVGLAAMHARRAAVQIWMDSRPTDEDLNE 234
Db 162 SLAFSCPTKPTKPTWYGATHLFNKNVFCAAVSRVAAAHAASDALMIDDLPTPTIEDLDR 221
OY 235 LIGITTIIVTYCEGKNLLQRLNELVNDVQDVDAATATGSR-----AASRPTRPRAPA 280
Db 222 FLKAAATRIILVCEGSKLEEMAN-----ATMERSPDGCAAAVAPRIGYDRRP- 265
OY 291 RSASRPR 297
Db 266 RLASRRR 272

```

RESULT 4
T42554
 legument protein - equine herpesvirus 4 (strain NS80567)
C:Species: equine herpesvirus 4
A:Variety: strain NS80567
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42554
R:TelFord, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J: Gen. Virol. 79, 1197-1203, 1998
A:Title: The DNA sequence of equine herpesvirus-4.
A:Reference number: Z22173; MUID:98264497
A:Accession: T42554
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-304 <TEL>
A:Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59525.1; PID:g26059535
A:Experimental source: strain NS80567
C:Genetics:
A:Gene: 11
C:Superfamily: varicella-zoster virus gene 9 protein

[illegible]

RESULT 5
S24228
BHV-1 protein homolog vZV9 - bovine herpesvirus 1 (fragment)
C.Species: bovine herpesvirus 1
C.Date: 09-Jun-1994 #sequence_revision 29-Aug-1997 #text_change 03-Nov-2000
C.Accession: S24228
R.Misra, V.
submitted to the EMBL Data Library, January 1992
A.Reference number: S24228

A:Accession: S24228
A:Molecule type: DNA
A:Residues: 1-195 <MIS>
A:Cross-references: EMBL:Z11610
C:Superfamily: varicella-zoster virus gene 9 protein

Query Match 15.7%; Score 245.5; DB 2; Length 195;
Best Local Similarity 32.1%; Pred. No. 4.4e-08;
Matches 62; Conservative 24; Mismatches 98; Indels 9; Gaps 3;

OY 99 ARAPEPPAGSGAGRTPTTAPRAPRTQVATKAPA-----AETTRGRKSAQPSAAL 153
DB 7 ARGRDRAAAAGTTVAAPAAPARSSSRPPRAADPPVLRPATRSGSGGAGAVAVG 66
OY 154 PDAPASTARTSKTPAQGLARKHSTAPNPDPAPPTPRVAGNKKVFCACAVRLLAAMA 213
DB 67 P--PRAPAPGANAASG--RPLAFSAAPKTPKAPWCPTHAAYNRTIFCEAVALVAEYA 122
OY 214 RMAAVQMDMSRPRTDEDNELLGITTVTCCEGKNLORANELVNPVODVDAATAT 273
DB 123 RQAASVWSDPPKSNERRDRMLKSAIRILVCEGSLAANDIILAAARQPARAGSTS 182
OY 274 RGRSAASRPTERP 286
DB 183 GGSRLRGERARP 195

RESULT 6
W2BE9
gene 9 protein - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C:Accession: J27212
R:Davidson, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A:Title: The complete DNA sequence of varicella-zoster virus.
A:Reference number: A27345; MUID:8630657
A:Accession: J27212
A:Molecule type: DNA
A:Residues: 1-302 <DAV>
A:Cross-references: EMBL:X04370; MID:g59989; PIDN:CAA27892.1; PID:g59998
C:Genetics:
A:Gene: 9
C:Superfamily: varicella-zoster virus gene 9 protein

Query Match 14.4%; Score 225.5; DB 1; Length 302;
Best Local Similarity 26.2%; Pred. No. 1e-06;
Matches 89; Conservative 27; Mismatches 107; Indels 117; Gaps 10;

OY 2 TSTRSVKSGP-----REVPDEYEDLYTPSSGMSAPSPDPTSRGALQ 46
DB 29 TARSRVVGPPDDSDSLGYTTVGADSPSPVADLYFEHKNTTPRHQPNDS----- 82
OY 47 TTSRQGEVRFVQYDESDYALYGGSSSEDDHEVPRTRR-----VSGAVLSGPGR 99
DB 83 -----GSEDDDEDDEVAARREARLRHLEVEDAYENPLSY 119
OY 100 RAPPPAGSGAGRTPTTAPRAPRTQVATKAPAAPAEETTRGRKSAQPSAALPDAPAS 159
DB 120 EXP-----SRSPTKNA-----VKRK-----LEDSP-K 141
OY 160 TAPTSKTPAQGLARKHSTAPNPDPAPPTPRVAGNKKRVCACAVRLLAAMHARAAYO 219
DB 142 RAPPGAGTASG--RPLSFSTAPKATATSSWCGPTPSYKRVCFCEAVRVAAMQAKRAA 199
OY 220 LMDMSRPRTDEDNELLGITTVTCCEGKNLORANE----- 257
DB 200 AAKNSNPFRNAELDRLLTCAVIRITVHEGLNLIQAANEADLGEAGSVSRGHNKKTGDIQ 259
OY 258 --LVNPDVVDVDAATATRGRSAASRPTERPAPARSASR 295

DB 260 GGMGNEMMYAQVRKPKSRDTDTQTGRITNRSR--ARSASR 297

RESULT 7
S60741

major tegument protein VP22 homolog - Marek's disease virus
C:Species: Marek's disease virus
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S60741
R:Kopidesova, D.; Kopacek, J.; Zelnik, V.; Ross, N.L.J.; Pastorekova, S.; Pastorek, Arch. Virol. 140, 355-362, 1995
A:Title: Identification and characterization of a cDNA clone derived from the Marek's A:Reference number: S60741; MUID:95225753
A:Accession: S60741
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-249 <KOP>
A:Cross-references: EMBL:X73370

Query Match 13.5%; Score 211; DB 2; Length 249;
Best Local Similarity 25.9%; Pred. No. 6.2e-06;
Matches 74; Conservative 33; Mismatches 93; Indels 86; Gaps 9;

OY 38 DTSRRCALGTRSRQGEVRFVQYDESDYALYGGSSSEDDHEVP-----RTRRPVSGA 91
DB 3 DSERRKSSERRS-----LGTPSAVD--VSTPARRSTKTRQRLNLD 42
OY 92 VLSGPGPARAPPPAGSGAGRTPTTAPRAPRTQV-ATKAPAAPAEETTRGRKSAQPS 150
DB 43 DLSKHGPFTHDP-----TQKYKSAKAVSEDSVSTTRGGFTNKP-- 80
OY 151 ALPDPASTAPTRSKTPAQGL-ARKLHSTAPNPDPAPPTPRVAGNKKRVCACAVRLLA 209
DB 81 -----RAKPGVAAVQSNKFAFSTAPSSASTWRSNTVAENRMFCGAAVATVA 127
OY 210 AMHARMAAVQMDMSRPRTDEDNELLGITTVTCCEGKNL-----LQ 253
DB 128 QYHAYGALALMRQDPPRTNEELDAFLSRVAVIKITIQEGPNLGEAETCARLLSEGLS 187
OY 254 RANELVNPVODVDAATATRG-----RSAASRPTERPAPARS 292
DB 188 QGNENVRKSKSERTTKSETRRGGEIEIKSPDDPSHRTNRPATYS 233

RESULT 8
JQ2201

UL49h protein - Marek's disease virus
C:Species: Marek's disease virus
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C:Accession: JQ2201
R:Yanagida, N.; Yoshida, S.; Nazertan, K.; Lee, L.F.
J. Gen. Virol. 74, 1837-1845, 1993
A:Title: Nucleotide and predicted amino acid sequences of Marek's disease virus homol A:Reference number: JQ2199; MUID:93389438
A:Accession: JQ2201
A:Molecule type: DNA
A:Residues: 1-249 <YAN>
A:Cross-references: GB:LI0283; MID:g388703; PIDN:AAA03148.1; PID:g388706
A:Experimental source: strain GA

Query Match 13.5%; Score 210; DB 2; Length 249;
Best Local Similarity 25.9%; Pred. No. 7.1e-06;
Matches 74; Conservative 33; Mismatches 93; Indels 86; Gaps 9;

OY 38 DTSRRCALGTRSRQGEVRFVQYDESDYALYGGSSSEDDHEVP-----RTRRPVSGA 91
DB 3 DSERRKSSERRS-----LGTPSAVD--VSTPARRSTKTRQRLNLD 42
OY 92 VLSGPGPARAPPPAGSGAGRTPTTAPRAPRTQV-ATKAPAAPAEETTRGRKSAQPS 150
DB 43 DLSKHGPFTHDP-----TQKYKSAKAVSEDSVSTTRGGFTNKP-- 80

QY 151 AALPDAPASTAPTRSKTPAAGL-ARKLHFTAPNDPAPTPRVAGFNKRVFCAAVGRLA 209
 C:Accession: S04713
 R:Cheung, A.K.
 Nucleic Acids Res. 17, 4637-4646, 1989
 A:Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies
 A:Reference number: S04713; PMID:89315207
 A:Accession: S04713
 A:Molecule type: DNA
 A:Residues: 1-1460 <CHE>
 C:Superfamily: herpesvirus immediate-early protein IE175
 C:Keywords: DNA binding; early protein; transcription regulation

QY 210 AMHARMAAVALMDMSRPDEDLNELLGTTITVYCEGNL-----LQ 253
 Db 128 QYHAYGALALMHODPPTNEELDAFRAVAVIKITIOEGNPLNGEAFETCARKLEESGLS 187

QY 254 RANELVNPVQDDAATATRG-----RSASRPTEPRAPARS 292
 Db 188 QGNNVKSXKSERTTKSERTRGGEIEIKSPDPGSHRNHRTATIS 233

RESULT 9
 OQBEJ
 BHLF1 protein - human herpesvirus 4 (strain B95-8)
 C:Species: human herpesvirus 4, Epstein-Barr virus
 C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 23-Aug-1997
 C:Accession: A03742
 R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
 Mol. Biol. Med. 1, 21-45, 1983
 A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
 A:Reference number: A93065; PMID:85055713
 A:Accession: A03742
 A:Molecule type: DNA
 A:Residues: 1-660 <BAN>
 R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
 Nature 310, 207-211, 1984
 A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
 A:Contents: annotation; protein coding region
 C:Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52
 C:Superfamily: human herpesvirus 4 BHLF1 protein

Query Match 10.3%; Score 161.5; DB 1; Length 660;
 Best Local Similarity 23.8%; Pred. No. 0.014;
 Matches 89; Conservative 21; Mismatches 133; Indels 131; Gaps 12;

QY 3 SRSVSGPREVPRDEEDLYTPSSGMASSPDPSTSRGALQTRSGRGEVRFVQYDE 62
 Db 87 SRSRRTGPAE-----QADHAHSNPTGGCSDPQSP-----KTRQG----- 123

QY 63 SDVLYGSSSEDD-----EHPVPTRRPVSGAVLSCGPAP----- 100
 Db 124 --VALGSGAGLGRGPRPHAFQVQMSARNPGCPRTWRRRSGAQRHPRPGAGQRPSP 181

QY 101 -----APPPA--GSGGAGRTPTTA-----PRAPRT 124
 Db 182 TGGRPAPAGAPGTTPAAGPVGGAAPVSGAPNHERGSGPADPPAARLPRERQEPRLPD 241

QY 125 ORVATKAPAP-----AAETTRGKSAQEPESALPDAP-----ASTAPTRSKTPAAGL 172
 Db 242 LAAAGKCPAPPTPTRSAAAOQTHRRPPGCRPSARNPGCCTRTWRNRSGAQRHPRPAGQ 301

QY 173 ARKLHFTAPNDPAPTPRVAGFNKRVFCAAVGRLAAMHARMAAVALMDMSRPDEDL 232
 Db 302 RPSGPTGAPAGAPGTTPAAGPVGCG--AAVSGATPHRSGSGADPPAARLPRER 358

QY 233 NELLGTTITVYCEGNLQANELVNPVQDDA-----TATRRSASRPTEP 265
 Db 359 QE-----PRLPDLLAAOQCPAGPPTTRSGAAAOQTHRR 392

QY 286 PRAPARSRRPR 299
 Db 393 PPGCPRSARNPGCP 406

RESULT 10
 EDBEIF
 Immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)
 C:Species: suid herpesvirus 1

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Feb-1997
 C:Accession: S04713
 R:Cheung, A.K.
 Nucleic Acids Res. 17, 4637-4646, 1989
 A:Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies
 A:Reference number: S04713; PMID:89315207
 A:Accession: S04713
 A:Molecule type: DNA
 A:Residues: 1-1460 <CHE>
 C:Superfamily: herpesvirus immediate-early protein IE175
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 10.3%; Score 161; DB 1; Length 1460;
 Best Local Similarity 23.5%; Pred. No. 0.033;
 Matches 92; Conservative 24; Mismatches 127; Indels 148; Gaps 17;

QY 3 SRSVSGPREVPRDEEDLYTP-----SSGMASSPDPSTSRGA 44
 Db 42 SRRGSSG-----EDLLFGGLFSDDAAEAAVLAAGATRRPRP-----SA 87

QY 45 LQTRSGRGEVRFVQYDESDYALYGSSSEDDHEVPTRRPVSGAV-----LSCP 96
 Db 88 QQGRHARGSGEIVLDD-----EEDEPGSPAAGSVGLSIRAPSTVTSSGP 138

QY 97 GPAPAPR-----PAGSGAGRTPTTAPRAPRTQVATYAPAAAEETRG-- 142
 Db 139 GGPAPAPGRRRRQNSQRRGPRPAAGAPRRPRRRPAPAPAPRRRGD 198

QY 143 -----RKSAQPE-----SAALPDAPASTAPTRSK-----T 167
 Db 199 PRGRTSRVSGRRRGIGRRHNSQRRWQRRHGGRLQRP--PRGSRKRRPAAAP 256

QY 168 PAQGLARKLHFTAPR-----NPDAPTPRVAGFNKRVFCAAVGRLAAMHARMA 216
 Db 257 PAEGTAVVTTTSTASPLDPRAPARLDPRAPARPERRLQPL-----QLQHNHRR 310

QY 217 AVQILMDMSRPTEDELLGTTITVYCEGNL-----LQANELVNPVQDDAAT 271
 Db 311 RAR-----RPRPR-----GRGTRPRRGAGRLQRRRRRAGE-----GA 347

QY 272 ATGR-----SAASRTERPRAPARSRRPR 299
 Db 348 LRKRGFSSTSSGSDSLSPARSPAPRAP 378

RESULT 11
 A45344
 Immediate-early protein - suid herpesvirus 1 (strain Kaplan)
 C:Species: suid herpesvirus 1
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: A45344
 R:Vitek, C.; Kozmik, Z.; Paces, V.; Schlrm, S.; Schwytzer, M.
 Virology 179, 365-377, 1990
 A:Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented
 A:Reference number: A45344; PMID:91021039
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1446 <VL>
 A:Cross-references: GB:M34651; NID:q334070; PIDN:AAA47470.1; PID:q334071
 C:Superfamily: herpesvirus immediate-early protein IE175
 C:Keywords: DNA binding; early protein; transcription regulation

Query Match 9.8%; Score 153.5; DB 1; Length 1446;
 Best Local Similarity 25.1%; Pred. No. 0.091;
 Matches 93; Conservative 35; Mismatches 129; Indels 113; Gaps 18;

QY 3 SRSVSGPREVPRDEEDLYTP-----SSGMASSPDPSTSRGA 44
 Db 41 SRRRGSSG-----EDLLFGGLFSDDAAEAAVLAAGATRRPRP-----SA 86

Oy 45 IOTRSRQGEVRFVQYDESD-----VALYGGSSSEDDHEPEV---PRT- 85
 Db 87 OOOOOPRRSGEIVLDDDEDEDERGSPAGSPGALHQS-----ENGLHVLGPRSA 141
 Oy 86 ---RPVSAVLSCG-----GPAPAP---PPAGSGAGRTPTTAPAPRTQVATKA 131
 Db 142 GSGPRPPPAALAAEAGAPGPGGRSSPSAASPASSSGSPG--PSAAPRRWSPARDDPVG 199
 Oy 132 PAAPAEETTRGRKSAQESALPDAPASTAPRTSKTPAGLAKLHFAAPPDPAPAP 191
 Db 200 EGPAPAPRTTAPAPAP--AAVAAAPARRGPASPSAPAGPV-----SAPGGGAP--- 248
 Oy 192 RVAGENKRVCAVGRLAAMHA-----RMAAVQLMD-----MSRPTDEDNEL 236
 Db 249 -SAGDR-----GRHHQHREPLIDEPAAARRIDPRRLGARSPPSSNPNNSNTTIV 300
 Oy 237 GTTTRVYCECKNLQARNELVNDPVVD-----VDAATATGCR---SAASRTERPPAP 289
 Db 301 AAVETARCGEKEDGIGLADGAPAPQRRRRRAGEGALRRGRCFSSSSSGSDSLSP 360
 Oy 290 ARSASRRAP 299
 Db 361 ARSPAPAP 370

RESULT 12

S52418
 GTP-binding regulatory protein Gs alpha-XL chain - rat
 N:Alternate names: G protein XL-alpha-s
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 02-Feb-2001
 C:Accession: S52418
 R:Kehlenbach, R.H.; Matthey, J.; Huttner, W.B.
 Nature 372, 804-809, 1994
 A:Title: XL-alpha-s is a new type of G protein.
 A:Reference number: S52418; MUID:95089824
 A:Accession: S52418
 A:Molecule type: mRNA
 A:Residues: 1-846 <KEH>
 A:Cross-references: EMBL:X84047; NID:9642267; PIDN:CA58866.1; PID:9642268
 R:Kehlenbach, R.H.; Matthey, J.; Huttner, W.B.
 Nature 375, 253, 1995
 A:Title: Correction: XLa1phas is a new type of G protein.
 A:Reference number: S58911
 A:Contents: annotation: assignment of start_codon
 A:Note: experimental data from this paper suggest that the translation is initiated at F
 C:Keywords: GTP binding; nucleotide binding; P-loop; signal transduction
 F:133-846/Product: GTP-binding regulatory protein Gs alpha-XL chain #status experimental
 F:499-506/Region: nucleotide-binding motif A (P-loop)
 F:744-747/Region: GTP-binding NKXD motif

Query Match 9.5%; Score 149; DB 2; Length 846;
 Best Local Similarity 24.6%; Pred. No. 0.099;
 Matches 78; Conservative 26; Mismatches 119; Indels 94; Gaps 12;

Oy 20 EDLYTTPS-----SGMASPDPDTSRSGALQTRSRQGEVRFVQYDESDYALYGGSSSD 75
 Db 90 ETVHKKPAVAESGTDSSKADPDSTHNAVLIQPEEVGV----- 129
 Oy 76 DEHPVPRTRPVS-----GAVLSGPPAPAPPPAGSGAGRTPTTAPAPRTQVATKA 131
 Db 130 ---PTMPTDLPAPSDAGDVRAEPDGTAPATPAESD--NDEPAAAAAEEPAEPAAP 185
 Oy 132 PAAPAEETTRGRKSAQESALPDAPAST-----APTRSKTPAGLAKLHFA 178
 Db 186 AAEPPAAE-----PAAEPAAEAAPDTEAESASGAVDPTQEPAAAAAASATPAEPAAR--- 236
 Oy 179 STAPNPDPAPMTPRVAGFKRVCAAV-----GRLAAMHMAAQAQLDMSRPTD 229
 Db 237 -AAPPTPEPATRAVPSARAHPAAGAVPGASMAAARAAARAAVAGPLV----- 287
 Oy 230 EDLNELAGITTRVYCECKNLQARNELVNDPVVDVDAATATR---GRSAASRPT- 284

Db 288 -----GARSISATPARASILPARAAAR-----AASARAVALVAGRSASAPSRSA 332
 Oy 285 ---RPPAPARSASRRPP 299
 Db 333 HLRPSPETIQVADPPRP 349

RESULT 13

H75457
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: H75457
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: H75457
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-395 <WHI>
 A:Cross-references: GB:AE001946; GB:AE000513; NID:96458655; PIDN:AAF10516.1; PID:9645
 C:Genetics:
 A:Gene: DR0938
 A:Map position: 1

Query Match 9.4%; Score 146.5; DB 2; Length 395;
 Best Local Similarity 25.1%; Pred. No. 0.065;
 Matches 80; Conservative 23; Mismatches 133; Indels 83; Gaps 13;

Oy 6 SVKSGREVPRDEYEDLYTPSSGMASPDSPDTSRSGALQTRSRQGEVRFVQYDESDY 65
 Db 44 SLLGERRAPAEVGV---APQPTTSIPVSPGAVVADSGSPQAAAPAAQATT----- 90
 Oy 66 ALYGGSSSEDDHEPEVPTRRRVSGAVLSGPPAPAPPPAGSGGAGRRP-----TTP 119
 Db 91 ---AGKIPPAAPAPAPKIPPPV-----PEPRRMAPAP-----TPPPEVETTYA 133
 Oy 120 RAPRTQVATKAPA-----APAEETTRGRKSAQESALPDAPASTAPRTSKTPAGQL 172
 Db 134 ASPTIQPYTQAPATQTPPTPQTPAAQAPATQPPAT--APEPAPEAPATPPEPAT-- 189
 Oy 173 ARKLHSTAPMPDAPMTPRVA-----GFNKRVCFAVGRLAAMHMAAQAQLDMS 224
 Db 190 -----PTEPAPAP-APGTPAVAPSAQRTPLRDYRMGLTGFSEALRSATAGV----- 236
 Oy 225 RPRTEDELNELLGITTRVYCECKNLQOR-----ANELVNDPVVDVDAATATRGSAA 280
 Db 237 -----SALGYVYAYIDL--GNQFVAVQVGFADGAGGQAAADIRAVARAEVLYPPR 285
 Oy 281 RPTPRPARASRRPP 299
 Db 286 GQTLNPPAPAAAAEAPATP 304

RESULT 14

F75518
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: F75518
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: F75518

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-839 <WHI>
 A:Cross-references: GB:AE001904; GB:AE000513; NID:g6458129; PIDN:AAFI0038.1; PID:g645814
 A:Experimental source: strain RL
 C:Genetics:
 A:Gene: DR0458
 A:Map position: 1
 C:Superfamily: herpesvirus immediate-early protein IE110; RING finger homology

Query Match 9.4%; Score 146; DB 2; Length 839;
 Best Local Similarity 22.3%; Pred. No. 0.15;

Matches 80; Conservative 35; Mismatches 104; Indels 140; Gaps 18;

OY 7 VKSGPREVPDEVEDLYTPSSGMASSPDSPDPT-----SRGALQTRSGRQGEVRFVQYDE 62
 DB 207 VQAPPTPTP-----PPQAAAPPTPMAPQTPATQAPAAQTPAAQ----- 246
 OY 63 SDYALYGSSSEDEDEHPVPTTRPVSGAVLSCGPAPAPPPAGS----- 108
 DB 247 -----APATQTPATP-APAAQRPAGAPSPAPAPQA-NAPAGSVPEATVPESTPA 297
 OY 109 GGAGRTPTTAPR-----APRTQRYATKAPAPAAETTRGR---KSAOPESAA----- 152
 DB 298 APSAQTPPTPTRETACTEASPAAPNSSAAPNBPASEPVAGPCTAASSPESASPVTVTP 357
 OY 153 ---LPDAPAST-----APTR-----KTPAQGLARKLHFSTAPPNPDAPWTP 191
 DB 358 RGETPPTAASAGTPSAGRTVPAPAPSPASEGASAKRTPGAG-----SOTPPIPATP--- 407
 OY 192 RVAGFKRVFCAVAGRLAAMHARMAAVQIWMDSRPR---TDDELNELLGITTTIRVTC 246
 DB 408 -----IPATPAGRSSSGSAGTAA-----ARPNAAPAVSEDSRSDVSGLPR----- 447
 OY 247 EGNLQIRANELVNPVDVDAATATRGSAASRPTERRA--PAR-----SASRPR 297
 DB 448 -----REDAPAESPPVAASPARGASSAPSAAPAAVPSRAVPSGGSVSAPR 493

RESULT 15

B87254

translation initiation factor IF-2 [Imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #cexl_change 10-May-2001

C:Accession: B87254

R.Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: B87254

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1037 <STO>

A:Cross-references: GB:AE005673; NID:g13421134; PIDN:AAK22030.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC0042

C:Superfamily: translation initiation factor IF-2; translation elongation factor Tu hom

Query Match 9.2%; Score 144; DB 2; Length 1037;
 Best Local Similarity 24.2%; Pred. No. 0.24;

Matches 79; Conservative 31; Mismatches 104; Indels 112; Gaps 14;

OY 54 EVR---FVQIDESDYALY--GSSSE--DDEHP-----EVPTRRPVSGAVLSC----- 95
 DB 2 EVRPGFLLTWNERRFSGVTPGGSTSERMSDENENGRPGRTPMTLKRQGSVSGAVYKQS 61
 OY 96 -----GPARAPPPAGSGAG----- 112
 DB 62 FSHGRTKTYVETKRTTHAPASGNLAAPSSAERRHGEAPAPRPAPPGGGGAGLSQ 121

OY 113 -----RTPTTAPRAPPTQRYATKA-----PAAPAAETTRGRKKSAPESALP-----D 155
 DB 122 EELRARGVVDAREAQARQVAAAEARARAAQAEAAKAAKAAERAAAAAPPPVAG 181
 OY 156 APASTAPTRSKTPTAOGIARKLHFSTAP---PNPDAPWTPRVAGFNKRVFCAVAGRLAAM 211
 DB 182 APAPAPAPADVTPPPAPAPQ-----APRPVQAAPVAPSAAPRQDAPQDTRAAAPGQ----- 231
 OY 212 HARMAAVQIWMDSRPTDEDLNELLGITTTIRVTCGKNLQIRANELVNPVDVDAAT 271
 DB 232 -----TRTPEPSRDRDRDPS-----TTYTRPAPQGDPRPNQRA---PRD-----AN 271
 OY 272 ATRGRSAASRPTERRPAPAPARSASRPR 297
 DB 272 ANFGQRAPREGRDPRGPRPDGDRPQ 297

Search completed: August 28, 2002, 12:24:24
 Job time: 233 sec

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OM protein - protein search, using sw model

Run on: August 28, 2002, 12:20:11 ; Search time 13.11 Seconds

(without alignments)
560,801 Million cell updates/sec

Title: US-09-522-278B-12

Perfect score: 1561

Sequence: 1 MTSRSRVKSGPREVPDEYE.....PTERRAPARSASRRPRVE 301

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
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5: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilltest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1561	100.0	301	US-08-303-861-21	Sequence 21, Appl
2	1561	100.0	301	US-09-011-073A-1	Sequence 1, Appl
3	1548	99.2	301	US-09-230-421-2	Sequence 2, Appl
4	1203.5	77.1	246	US-09-336-093-5	Sequence 5, Appl
5	573	36.7	144	US-09-420-421-3	Sequence 3, Appl
6	271.5	17.4	258	US-08-303-861-18	Sequence 18, Appl
7	271.5	17.4	258	US-08-303-861-19	Sequence 19, Appl
8	271.5	17.4	258	US-09-213-343-2	Sequence 2, Appl
9	225.5	11.4	302	US-08-303-861-20	Sequence 20, Appl
10	172.5	11.1	139	US-08-680-726A-66	Sequence 66, Appl
11	172.5	11.1	139	US-09-092-409-66	Sequence 66, Appl
12	169	10.8	34	US-09-011-073A-2	Sequence 2, Appl
13	166	10.6	32	US-09-230-421-14	Sequence 14, Appl
14	142.5	9.1	263	PCR-US91-06532-2	Sequence 26, Appl
15	141	9.0	258	US-08-483-533-26	Sequence 26, Appl
16	141	9.0	258	US-09-283-471A-26	Sequence 26, Appl
17	141	9.0	264	US-08-483-533-40	Sequence 40, Appl
18	141	9.0	264	US-09-283-471A-40	Sequence 40, Appl
19	136.5	8.7	355	US-08-483-533-41	Sequence 41, Appl
20	136.5	8.7	355	US-09-283-471A-41	Sequence 41, Appl
21	136.5	8.7	355	PCR-US91-06532-3	Sequence 3, Appl
22	131.5	8.4	661	US-08-795-868-14	Sequence 14, Appl
23	131.5	8.4	661	US-09-303-069-14	Sequence 14, Appl
24	130.5	8.4	591	US-09-082-737-2	Sequence 2, Appl
25	129.5	8.3	252	US-08-483-533-43	Sequence 43, Appl
26	129.5	8.3	252	US-09-283-471A-43	Sequence 43, Appl
27	128	8.2	882	US-09-413-814-78	Sequence 78, Appl

28	127.5	8.2	404	US-09-232-468A-8	Sequence 8, Appl
29	126.5	8.1	1298	US-08-690-473-2	Sequence 2, Appl
30	126.5	8.1	1298	US-09-259-821A-2	Sequence 2, Appl
31	126.5	8.1	1298	US-08-843-659-2	Sequence 2, Appl
32	122	7.8	265	US-09-199-637A-369	Sequence 369, App
33	120	7.7	1060	US-08-931-820-3	Sequence 3, Appl
34	120	7.7	1418	US-08-963-825-20	Sequence 20, Appl
35	120	7.7	1418	US-09-010-999-1	Sequence 1, Appl
36	120	7.7	1418	US-09-570-573-20	Sequence 20, Appl
37	120	7.7	1418	US-09-548-608-20	Sequence 20, Appl
38	119.5	7.7	169	US-08-483-533-28	Sequence 28, Appl
39	119.5	7.7	169	US-09-283-471A-28	Sequence 28, Appl
40	118	7.6	1426	US-09-136-574A-43	Sequence 43, Appl
41	118	7.6	1442	US-08-316-650-12	Sequence 12, Appl
42	118	7.6	1442	PCR-US95-02251-12	Sequence 12, Appl
43	117	7.5	20	US-09-230-421-6	Sequence 6, Appl
44	116	7.4	507	US-08-860-635A-19	Sequence 19, Appl
45	116	7.4	507	US-09-281-476-19	Sequence 19, Appl

ALIGNMENTS

```
RESULT 1
US-08-303-861-21
; Sequence 21 Application US/08303861
; Patent No 6086902
; GENERAL INFORMATION:
; APPLICANT: ZAMB, TIMOTHY
; APPLICANT: LIANG, XIAOPING
; APPLICANT: BABIUK, LORNE A.
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
; TITLE OF INVENTION: VACCINES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,861
; FILING DATE: 09-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 29310-20020.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEEX: 706141
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-303-861-21

Query Match 100.0%; Score 1561; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.7e-127;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MTSRSRVKSGPREVPDEYEDLYTPSSGMASSPDDTSRRGALQTRSGRGEVRFVQY 60
|||||
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Db 1 MTSRRSVKSGPREVPDEYEDLYTTPSSGMSAPSPDPSRRGALOTRSRQGEVRFVQY 60
QY 61 DESDYALVGGSSSEDEHPEVPTRRPVSGAVLSGPGAPAPPAGSGAGTPTTAPR 120
Db 61 DESDYALVGGSSSEDEHPEVPTRRPVSGAVLSGPGAPAPPAGSGAGTPTTAPR 120
QY 121 APPTORVATKAPAPAAETTRGRKSAQPEESALPDAPASTAPTRSKTPAOGCLARKLHFTST 180
Db 121 APPTORVATKAPAPAAETTRGRKSAQPEESALPDAPASTAPTRSKTPAOGCLARKLHFTST 180
QY 181 APPNPDAWPTPRVAGFENKRVFCAVGRLLAMHARMAAVOLMDMSRPTDEDLNELLGITTT 240
Db 181 APPNPDAWPTPRVAGFENKRVFCAVGRLLAMHARMAAVOLMDMSRPTDEDLNELLGITTT 240
QY 241 IRVTVEGKNLLOLANELVNPVVDVDDATATRGSAASRPTERRPAPARSASRPRPV 300
Db 241 IRVTVEGKNLLOLANELVNPVVDVDDATATRGSAASRPTERRPAPARSASRPRPV 300
QY 301 E 301
Db 301 E 301

RESULT 2

US-09-011-073A-1
; Sequence 2 Application US/09011073A
; Patent No. 6184038
; GENERAL INFORMATION
; APPLICANT: Ochrone et al.
; TITLE OF INVENTION: TRANSPORT PROTEINS AND THEIR USES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESS: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 7.0 & ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,073A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/01831
; FILING DATE: JULY 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Earp, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 5759-49294/DJTE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-011-073A-1

Query Match 100.0%; Score 1561; DB 4; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.7e-127;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEYEDLYTTPSSGMSAPSPDPSRRGALOTRSRQGEVRFVQY 60
Db 1 MTSRRSVKSGPREVPDEYEDLYTTPSSGMSAPSPDPSRRGALOTRSRQGEVRFVQY 60
QY 61 DESDYALVGGSSSEDEHPEVPTRRPVSGAVLSGPGAPAPPAGSGAGTPTTAPR 120
Db 61 DESDYALVGGSSSEDEHPEVPTRRPVSGAVLSGPGAPAPPAGSGAGTPTTAPR 120
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Db 121 APPTORVATKAPAPAAETTRGRKSAQPEESALPDAPASTAPTRSKTPAOGCLARKLHFTST 180
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Db 181 APPNPDAWPTPRVAGFENKRVFCAVGRLLAMHARMAAVOLMDMSRPTDEDLNELLGITTT 240
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Db 241 IRVTVEGKNLLOLANELVNPVVDVDDATATRGSAASRPTERRPAPARSASRPRPV 300
QY 301 E 301
Db 301 E 301

RESULT 3

US-09-230-421-2
; Sequence 2 Application US/09230421
; Patent No. 6200577
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: ANTI-HERPESVIRAL AGENTS AND ASSAYS
; FILE REFERENCE: P18189C
; CURRENT APPLICATION NUMBER: US/09/230,421
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 301
; TYPE: PRT
; ORGANISM: HERPESVIRUS TYPE 1
; US-09-230-421-2

Query Match 99.2%; Score 1548; DB 4; Length 301;
Best Local Similarity 99.3%; Pred. No. 2.3e-126;
Matches 299; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTSRRSVKSGPREVPDEYEDLYTTPSSGMSAPSPDPSRRGALOTRSRQGEVRFVQY 60
Db 1 MTSRRSVKSGPREVPDEYEDLYTTPSSGMSAPSPDPSRRGALOTRSRQGEVRFVQY 60
QY 61 DESDYALVGGSSSEDEHPEVPTRRPVSGAVLSGPGAPAPPAGSGAGTPTTAPR 120
Db 61 DESDYALVGGSSSEDEHPEVPTRRPVSGAVLSGPGAPAPPAGSGAGTPTTAPR 120
QY 121 APPTORVATKAPAPAAETTRGRKSAQPEESALPDAPASTAPTRSKTPAOGCLARKLHFTST 180
Db 121 APPTORVATKAPAPAAETTRGRKSAQPEESALPDAPASTAPTRSKTPAOGCLARKLHFTST 180
QY 181 APPNPDAWPTPRVAGFENKRVFCAVGRLLAMHARMAAVOLMDMSRPTDEDLNELLGITTT 240
Db 181 APPNPDAWPTPRVAGFENKRVFCAVGRLLAMHARMAAVOLMDMSRPTDEDLNELLGITTT 240
QY 241 IRVTVEGKNLLOLANELVNPVVDVDDATATRGSAASRPTERRPAPARSASRPRPV 300
Db 241 IRVTVEGKNLLOLANELVNPVVDVDDATATRGSAASRPTERRPAPARSASRPRPV 300
QY 301 E 301
Db 301 E 301

RESULT 4
US-09-336-093-5
Sequence 5, Application US/09336093A
Patent No. 6348185
GENERAL INFORMATION:
APPLICANT: Washington University School of Medicine
TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL
FILE REFERENCE: WSHU 2001
CURRENT APPLICATION NUMBER: US/09/336,093A
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 5
LENGTH: 246
TYPE: PRT
ORGANISM: Herpes simplex virus VP22 protein
US-09-336-093-5

Query Match 77.1%; Score 1203.5; DB 4; Length 246;
Best Local Similarity 80.7%; Pred. No. 1e-96; Indels 55; Gaps 2;
Matches 243; Conservative 0; Mismatches 3; Indels 55; Gaps 2;

QY 1 MTSRSVSGPREVPDEDELYTPSSGMA SPSPDTSRGALQTRSGEVEFYQ 60
DB 1 MTSRSVSGPREVPDEDELYTPSSGMA SPSPDTSRGALQTRSGEVEFYQ 60
QY 61 DESDYALYGSSSEDEDEHVEVPRTRPVSGAVLSGPGAPAPPPAGSGAGRTPTTAPR 120
DB 61 DESDYALYGSSSEDEDEHVEVPRTRPVSGAVLSGPGAPAPPPAGSGAGRTPTTAPR 120
QY 121 APRTQVATKAAAPAEETTRGRKSAQPSALPAPASTARTSKTPAQGLAKLHFT 180
DB 121 APRTQVATKAAAPAEETTRGRKSAQPSALPAPASTARTSKTPAQGLAKLHFT 180
QY 181 APPNDAPWTPRVAGFNKRVCAVGRLLAAMHAAVQUMDSRPRTDEDLNELLGIT 240
DB 181 APPNDAPWTPRVAGFNKRVCAVGRLLAAMHAAVQUMDSRPRTDEDLNELLGIT 240
QY 241 IRVTVCEGKLLQRLANELNPDVQVDAATATRGSAASRPTERRAPARSARRPV 300
DB 241 IRVTVCEGKLLQRLANELNPDVQVDAATATRGSAASRPTERRAPARSARRPV 300
QY 301 E 301
DB 246 E 246

RESULT 5
US-09-230-421-3
Sequence 77 Application US/09230421
Patent No. 6200577
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: ANTI-HERPESVIRAL AGENTS AND ASSAYS
FILE REFERENCE: P18189C
CURRENT APPLICATION NUMBER: US/09/230,421
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 144
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDES DERIVED FROM THE VP22TRUNC
US-09-230-421-3

Query Match 36.7%; Score 573; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.7e-42; Indels 0; Gaps 0;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 ASTAPTSTKTPAQGLARKLHFTAPNDPAPPTPVAGFNKRVCAVGRLLAAMHAA 217
DB 22 ASTAPTSTKTPAQGLARKLHFTAPNDPAPPTPVAGFNKRVCAVGRLLAAMHAA 81
QY 218 VOLMDSRPRTDEDLNELLGITTRVTVCEGKLLQRLANELNPDVQV 267
DB 82 VOLMDSRPRTDEDLNELLGITTRVTVCEGKLLQRLANELNPDVQV 131

RESULT 6
US-08-303-861-18
Sequence 18, Application US/08303861
Patent No. 6086902
GENERAL INFORMATION:
APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,861
FILING DATE: 09-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 29310-20020, 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-303-861-18

Query Match 17.4%; Score 271.5; DB 3; Length 258;
Best Local Similarity 31.2%; Pred. No. 4e-16; Indels 45; Gaps 8;
Matches 81; Conservative 25; Mismatches 109; Indels 45; Gaps 8;

QY 61 DESDY-----ALVGGSSSEDEDEHVEVPRTRPVSGAVLSGPG-----A 99
DB 10 DEDDYEDLWVRENSLDYEGSDHYEELR-----AATSGPEPSGRASVACAS 62
QY 100 RAPPAGSG-----GAGRT---PTTAPRAPRTQVATKAPAPAP-----ATTGRKSA 146
DB 63 AAAYGPAAAGRRRAAAAGTTVAAPAAAPARRSSASRPPRAADPPVLRATRGSSGG 122
QY 147 QPESALPDAPASTAPTSTKTPAQGLARKLHFTAPNDPAPPTPVAGFNKRVCAV 206
DB 123 AGAVAVGP--PPRAPAPGANAVASG--RPLAFSAAPKTPKAPWCGPTAYNRTICFAVA 178

OY 207 RLAAAHARAATAVOALMDMSRPTDEDINELLGTTITVTCCEGKNNLORANELVNPVOD 266
DB 179 LVAAEYARQAASVWSDPDKSNERLDRMLKSAIRILVCEGSGLLAANDILAARAORP 238
OY 267 VDAATATRGSAASRPTERP 286
DB 239 AARGSTSGESRLRGERARP 258

RESULT 7

US-08-303-861-19
Sequence 19, Application US/08303861
Patent No. 6086902
GENERAL INFORMATION:
APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,861
FILING DATE: 09-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 29310-20020.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-861-19

Query Match 17.4%; Score 271.5; DB 3; Length 258;
Best Local Similarity 31.2%; Pred. No. 46-16;
Matches 81; Conservative 25; Mismatches 109; Indels 45; Gaps 8;

OY 61 DESDY-----ALYGGSSSEDEHPEVPTTRRPVSGAVLSGPGP-----A 99
DB 10 DEDDYSDLVWRENSLYDESGSDHYEELR-----AATSGPEPGRASVACAS 62
OY 100 RAPPAGSG-----GAGRT---PTTAPRAPRTQVATKAPAPA-----AETTRGRKSA 146
DB 63 AAQVOPARGRDRRAAAGTTVAAPAPARRSSSRASRPRAADPPVLRPATRGSSCG 122
OY 147 QPESALPDAPASTARTKSTPAQGLARKLHFTAPNPDAPTPRVAGNKKVFCFAAG 206
DB 123 AGAVAAVGP--PRRAPPGANAASG--RPLAFSAARKTPKAPWCPTTHAVNRTIFCEAVA 178
OY 207 RLAAAHARAATAVOALMDMSRPTDEDINELLGTTITVTCCEGKNNLORANELVNPVOD 266
DB 179 LVAAEYARQAASVWSDPDKSNERLDRMLKSAIRILVCEGSGLLAANDILAARAORP 238

OY 267 VDAATATRGSAASRPTERP 286
DB 239 AARGSTSGESRLRGERARP 258

RESULT 8

US-09-213-343-2
Sequence 2, Application US/09213343
Patent No. 6316252
GENERAL INFORMATION:
APPLICANT: Harms, Jerome S.
APPLICANT: Splitter, Gary A.
TITLE OF INVENTION: Biotherapeutic Delivery System
FILE REFERENCE: 960296.95364
CURRENT APPLICATION NUMBER: US/09/213,343
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 258
TYPE: PRT
ORGANISM: Bovine herpesvirus.1
US-09-213-343-2

Query Match 17.4%; Score 271.5; DB 4; Length 258;
Best Local Similarity 31.2%; Pred. No. 46-16;
Matches 81; Conservative 25; Mismatches 109; Indels 45; Gaps 8;

OY 61 DESDY-----ALYGGSSSEDEHPEVPTTRRPVSGAVLSGPGP-----A 99
DB 10 DEDDYSDLVWRENSLYDESGSDHYEELR-----AATSGPEPGRASVACAS 62
OY 100 RAPPAGSG-----GAGRT---PTTAPRAPRTQVATKAPAPA-----AETTRGRKSA 146
DB 63 AAQVOPARGRDRRAAAGTTVAAPAPARRSSSRASRPRAADPPVLRPATRGSSCG 122
OY 147 QPESALPDAPASTARTKSTPAQGLARKLHFTAPNPDAPTPRVAGNKKVFCFAAG 206
DB 123 AGAVAAVGP--PRRAPPGANAASG--RPLAFSAARKTPKAPWCPTTHAVNRTIFCEAVA 178
OY 207 RLAAAHARAATAVOALMDMSRPTDEDINELLGTTITVTCCEGKNNLORANELVNPVOD 266
DB 179 LVAAEYARQAASVWSDPDKSNERLDRMLKSAIRILVCEGSGLLAANDILAARAORP 238
OY 267 VDAATATRGSAASRPTERP 286
DB 239 AARGSTSGESRLRGERARP 258

RESULT 9

US-08-303-861-20
Sequence 20, Application US/08303861
Patent No. 6086902
GENERAL INFORMATION:
APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30